

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2006, 13:13:43 ; Search time 259 Seconds
(without alignments)
5497.401 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	140	3.4	2668	3	US-09-031-606-11
4	140	3.4	2668	3	US-09-057-969-1
5	139	3.4	4411529	3	US-09-103-840A-1
6	136.5	3.4	2631	2	US-08-436-664-33
7	136.5	3.4	2631	3	US-09-135-642-33
8	136.5	3.4	2631	3	US-08-394-232A-33
9	136.5	3.4	2631	6	PCT-US95-04080-33

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11	134.5	3.3	2631	2	US-08-436-664-31	Sequence 31, Appl
12	134.5	3.3	2631	3	US-09-135-642-21	Sequence 21, Appl
13	134.5	3.3	2631	3	US-09-135-642-31	Sequence 31, Appl
14	134.5	3.3	2631	3	US-08-394-232A-21	Sequence 21, Appl
15	134.5	3.3	2631	3	US-08-394-232A-31	Sequence 31, Appl
16	134.5	3.3	2631	6	PCT-US95-04080-21	Sequence 21, Appl
17	134.5	3.3	2631	6	PCT-US95-04080-31	Sequence 31, Appl
18	134.5	3.3	2761	2	US-08-436-664-19	Sequence 19, Appl
19	134.5	3.3	2761	3	US-09-135-642-19	Sequence 19, Appl
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21	134.5	3.3	2761	6	PCT-US95-04080-19	Sequence 19, Appl
22	134.5	3.3	33529	3	US-09-144-085-3	Sequence 3, Appl
23	134	3.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl
24	133.5	3.3	3783	3	US-09-949-016-2647	Sequence 2647, App
25	132	3.2	5588	3	US-09-902-540-621	Sequence 621, App
26	131.5	3.2	3585	2	US-08-680-326-28	Sequence 28, Appl
27	131.5	3.2	124884	3	US-09-661-596A-76	Sequence 76, Appl
28	131.5	3.2	124884	3	US-09-913-514-1	Sequence 1, Appl
29	131.5	3.2	124884	3	US-10-288-823-76	Sequence 76, Appl
30	129.5	3.2	2715	3	US-09-712-363-101	Sequence 101, App
31	128.5	3.2	6790	2	US-08-418-893D-22	Sequence 22, Appl
32	128.5	3.2	125157	3	US-09-913-514-2	Sequence 2, Appl
33	127.5	3.1	3162	3	US-09-252-991A-8094	Sequence 8094, App
34	126.5	3.1	7419	3	US-09-252-991A-481	Sequence 481, App
35	126.5	3.1	7449	3	US-09-252-991A-396	Sequence 396, App
36	126	3.1	77536	3	US-09-410-551B-1	Sequence 1, Appl
37	125.5	3.1	77536	3	US-09-940-316B-1	Sequence 1, Appl
38	125.5	3.1	3150	3	US-09-252-991A-727	Sequence 727, App
39	125.5	3.1	19068	3	US-09-902-540-1123	Sequence 1123, App
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43	123.5	3.0	1664976	3	US-08-916-421B-1	Sequence 1, Appl
44	123.5	3.0	1664976	3	US-09-692-570-1	Sequence 1, Appl
45	123	3.0	2496	2	US-08-073-384C-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-418-893D-25
; Sequence 25, Application US/08418893D
; Patent No. 5559220
; GENERAL INFORMATION:
; APPLICANT: ROESSLER, PAUL G
; APPLICANT: OHLROGER, JOHN B
; TITLE OF INVENTION: GENE THAT ENCODES ACETYL-COENZYME A
; TITLE OF INVENTION: CARBOXYLASE FROM CYCLOSTELLA CRYPTICA
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: NATIONAL RENEWABLE ENERGY LABORATORY
; STREET: 1617 Cole Blvd.
; CITY: Golden
; STATE: CO
; COUNTRY: USA
; ZIP: 80401-3393
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,893D
; FILING DATE: April 7, 1995
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,938
; FILING DATE: September 14, 1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: O'CONNOR, EDNA
; REGISTRATION NUMBER: 29,252

Oy	517	IleGlyAlaGluHisValIleValIysAlaSerIleMetGlnIleA-	-----	529
Dd	1885	GThGCCACGTGAAGAAATTAAAGATCGTTTGCAAAAGAACAAGTCCTCACTGCAGGAGATT	 ::: :::	1944
Oy	529	-----	-----	529
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Oy	530	LeuGlnIlySValPheProSerArgTyrrThrAspArgAsnSerAlaGluProIlyAspVal	 ::: :::	549
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Oy	550	GInGIuTr	-----	552
Dd	2065	GAAGTATCCCAAACCGCTGAGAGACACTTTTGGCACTTTGGAGAGAGACTACTGT	 ::: :::	2124
Oy	553	ValPheSerValAsp--ProValGlyAsnAsnValGlyArgAspGlyIu-	-----	568
Dd	2125	ATCTTTGGTATGAGGAACCACTTGCGCTTGACATGTCATGGACGGGGCAACTGTCCGA	 ::: :::	2184
Oy	569	--ProGlyValPheIleAlaGluAlaValArgProSer-----Glu	 ::: :::	581
Dd	2185	ATGCCAACAAATTTTGAACCCCTCTGAACCTCCGCACTGATGTGACTGAAAGTTGTGCT	 ::: :::	2244
Oy	582	AasnPheGluThrAsnAspTyrrAlaIleArgAlaGlyValSerGluSerSerValAspGlu	 ::: :::	601
Dd	2245	TACCTCCAAACAAAGAGCAACTGTGAAGCGGC-----CAG	 ::: :::	2284
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Dd	2284	CCCATATCGAGGTTGAAGCGCATGAAGATGATC-----ATGCCAATCAAGCTACTGAG	 ::: :::	2334
Oy	622	AlaGlyValAlaIleGlyLeuIleSerLeuPheSerGlnLysTyrrPheLeuLysSerSer	 ::: :::	641
Dd	2338	TCTGGA-----AAATTACTCACAACTTAAGTCTGCA	 ::: :::	2370
Oy	642	SerSerPheGlnArgLysAspMetValSerSerMetGlu---SerAspValAlaThrIle	 ::: :::	660
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Oy	661	GlySerVal-----ArgAlaAspAspSerGluAlaLeuProArgMetAsp	 ::: :::	675
Dd	2431	AAGAAATATGAACCTTTTCCGGCAAAATTCGACATTATGAATGCAAGGTCGACTTGA	 ::: :::	2494
Oy	676	AlaArgThrAla--GluAsnIleValSerLysTyrrGlnLysIleLysSerLeuAlaPhe	 ::: :::	694
Dd	2491	CCGCGAAGACGATCATGATGTCCCTCTC-----GGGTTC	 ::: :::	2524
Oy	695	GlyProAspRHisArgIleGluMetLeuProGluValIleuAspGlyArgMetLeuLysIle	 ::: :::	714
Dd	2527	AACTTAGAC-----CCTGAGGCACTTGGCGGACGACCAACCAATTATACAGT	 ::: :::	2566
Oy	715	TryThrAspArgAlaAlaGluThrAlaGluLeuGlyLeuValTyrrAsp---TyrrThrIleu	 ::: :::	733
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Oy	734	LeuLysIleuSerValAspSerValThrValSerAlaAspGlyThrArgAlaLeuValGlu	 ::: :::	753
Dd	2629	GTTGCAATCTCAAGTTGATGCTGTGCT---ATCGCTGATGATGTTGTCCGCACTCTCACCAAA	 ::: :::	2685
Oy	754	AlaThrIleuGluGluSerAlaCysIleuSerAspIleuValHisProGluIleuAsnAla	 ::: :::	772
Dd	2686	GCGAAACACCGAG-----ACACTGAATGTGTATCTCCGAAGAACTTGGCC	 ::: :::	2730

RESULT 2
US-08-461-775-11
; Sequence 11, Application US/08461775
; Patent No. 5856773
; GENERAL INFORMATION:
; APPLICANT: MACODIER, Philippe
; APPLICANT: GUGLIENT, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION

```

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathie
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,775
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feuury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2668 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-461-775-11
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Best Local Similarity: 35.1% Conservative: 106
Query Match: 19.9% Mismatches: 255
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QY 67 ThrAlaThrLeuValSerLeuProProSerIleAspArg---ProGluArgHisValPro 85
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QY 86 -----IlEPoIIeaPheIeYrgInValLeuGlAlaGln 97
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QY 98 ThrHisPhe-----LeuThrAspGlyIleArgArgAlaPheGluAla 111
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QY 112 ArgValSerLyProProGlnPheNegIyPheSerAspAlaLeuIleSerArgArgGln 131
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Qy      145  SerArg-----ArgLyuTrpArgnLyuLyuLeuLeuAspArgLyuLyuLa  159
Db      948  GCGCGCAACGTCGTCATCGACAGAAAGTTCCGGCGCCGACCATCAACCAACGCGCGTC  1007
Qy      160  ThrValIleThrAspVal-----ProTyrAspLysValProGlyValLeuCyS  175
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Qy      176  -----ValLeuGlnGlnGlyGlyLyuTrpGlnIleVal  186
Db      1068  AAGAGGTGGGACCAAGCAACCAACATCGCGGGGTGACGCAACCAACCGCAGCGTG  1127
Qy      187  LeuArgValGlyGlnValLeuLeuLyuArgLyuTrpLeu-----  198
Db      1128  CTG-----GCCACGCGCTGGTCCGCGAGGCGCTGCGCAACGTCGCGCGCGCTCC  1181
Qy      199  ProLysSerPheLysGlnAspVal-----ValLeuValMetAlaLeuAlaPheLeu  215
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Qy      216  AspValSerArgAsp-----AlaMetAlaLeuAspPro  226
Db      1242  GACACCGCGCGCGCATCGACGACAAAGTCGACATCGCGCGCGCTGCTCCGCG  1301
Qy      227  ProAspPheIleThrGlyTrpLyuPheValGlnGlnValAlaLyuLyuLeuGlnLyu  246
Db      1302  CAGGCAAGCAAGTGGC---GAGCTCATCGCGCGCGATGACAAAGTGGCGGCAAGAC  1358
Qy      247  GlyAlaSerSerLeuAlaProAspLeuArgAlaGlnIleAspGlnThrLeuGlnLyu  265
Db      1359  GGTGCATCAACGTCGAGAGATCCCAACACTTCGCTGCTGACCTGACCTTCCACGAGGC  1418
Qy      266  -----IleThrProArgTrpValLeu-----GluLeuLeuGly  276
Db      1419  ATGGCTTCGACAAAGGCTACTGTCGCCGTACATGTGACCGACCAAGAGGATGAG  1478
Qy      277  LeuProLeuGlnLyuAspTrpLysAlaLysArgLeuLeuLeuLeuSerGlyValArgAsn  296
Db      1479  GCGGCTTCGACGACCGGTACATCTGATCCACAGGCGCAAGATGCTTCGACAGAC  1538
Qy      297  IleLeu-----  298
Db      1539  CTGCTCGCGCTGCTGGAAGGTCAATCCAGCGGGTGGCTCCAAGCCGCTGTCATC  1598
Qy      299  ---TrpSerValGlyGlyGlyLysAlaSerAlaLeuValGlyGlyLeuThrArgLyu  317
Db      1599  GCCGAGGACGTCGAGGGGAGGCGCGCTGTCGACCTGTGTGTCACAAAGATCCGCGCAG  1658
Qy      318  PheMetAsnGlnVal-----PheLeuArgMetThrAlaIleGlnVal  332
Db      1659  TTCACGCGCGTGGCGTCAAGGCGCGCGCTTCGCTGACCGCGCGCAAGCGATGCTCGGC  1718
Qy      333  AspLeuPheValAlaThrProSerAsnIleProAlaGlnSerPheGlnValTrpGlnVal  352
Db      1719  GACATGGCCACCTCAACGCGGTCCACCGCTCATCGCGAG-----GAGGTC  1763
Qy      353  AlaLeuAlaLeu-----ValAlaGlnAlaPheIle  362
Db      1764  GCGCTCAAGCTGACCAAGCGCGGTCTGACGTCGTGGGACCGCGCGCGCTCAACCTGC  1823
Qy      363  GlyLysLysProIleLeuLeuGlnLysAlaLysArgLysGlnPheGlnLeuGlnLysAla  382
Db      1824  ACCAAGGACGACACGACCATCTGTGACCTTGAGAAAGGACGCGCGAGACCTCCAGGCGC  1880
Qy      383  LysValMetAlaMetGlnIleProAlaMetLeuTrpAspTrpArgAsnAspTrpGlnIle  402
Db      1881  -----CGGTCGCCCAAGTCAAGGCGCAGATCGAGTCAACGACCTCGAGCGGACCGC  1934
Qy      403  AspPheGlyLeuGlnLys-----GlyLeuCyAlaLeuLeuIleGly  416

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Qy      417  LysValAspGluCyArgMetTrpLeuGlyLeuAspSerGlnAspSerGlnTrpArg---  435
Db      1995  GCGGCACCGAG-----GTCAAGCTGAAGAGCGGACACCATCGTCTG  2036
Qy      436  -----AsnProAlaIleValGlnPheValIleLeuAsnSerAsn  448
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Qy      449  Arg-----AspAsn-----AspAsp  454
Db      2097  TCCGCGCTGTCCACGCGCTGACAGTCTGTGACACAACTTCGCGCGCAGCGCGAGCTG  2156
Qy      455  LeuProGlyLeuCyLysLeuLeuGlnThr-----TrpLeuAla---  467
Db      2157  GCCACCGGTGTGCGGTGTCTCCGCGCGCGCGCTGACGCGCGCTCGCTGATGCGCAG  2216
Qy      468  -----GlyValValPheProArgPheArgAspThrLysAspLysLysPhe  482
Db      2217  AACGCGCGCTGAGAGGCTAGTCAATC-----ACCACCAAGTGGCGGAGCTC  2264
Qy      483  LysLeuGlyAsp-----TyrTyrAspAspPrometValLeuSer  495
Db      2265  GACAAAGGCGCAGGCTTCAACGCGCGCACCGCGAGTACGCGCGCTGTGTAAGCGCGC  2324
Qy      496  TyrLeuGlnArgValGlnValValGlnLysProLeuAlaAlaAlaThrMetAla  515
Db      2325  GTCAATCAACCGGTCAAGTCAACCGC---TCCGCGCTGAGAAACGCGCGCTTCATCGC  2381
Qy      516  ArgIleGlyAlaGlnIleValLysAlaSerAlaMetGlnAlaLeuGlnLysVal-PhePr  535
Db      2382  -----TCCGTCTCTGACGACCGCAACCTGTGTC  2411
Qy      535  GSerArgTrpThrAspArgAsnSerAlaGlnProLysAspValGlnGlnThrValPhe  555
Db      2412  GTCCAGGAAGCGCGCGCGAGAGAGCGCGGCTGTCACGGTCAACGCGCAGCAACCTGA  2471
Qy      555  rValAspProValGlyAsnAsn-----ValGlyArgAspGlyLysProGlyVal  571
Db      2472  GCGTACCCCTTCCGCGACCGAGCGCGGCTCCCGTGGGGAGCGGGCGCTC  2526

RESULT 3
US-09-031-606-11
; Sequence 11, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIERI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22131-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990

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```

ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2668 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-031-606-11

Alignment Scores:
Pred. No.: 7,95e-05 Length: 2668
Score: 140.00 Matches: 139
Percent Similarity: 35.1% Conservative: 106
Best Local Similarity: 19.9% Mismatches: 255
Query Match: 3.4% Indels: 139
DB: 3 Gaps: 34

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DB 567 CGCTGACGTCAGACCGGCGCGCTGCTGTACAGCAGGACCGGCGCGGACGTC 626
QY 47 LeuSerAspPheAsnPheThrSerAspSerSerSerPheAlaThrAlaThrThr 66
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QY 176 -----ValLeuGlnGluGlyGlyGluThrGluIleVal 186
DB 1068 AAGAGGTGCGACCAAGACCAACGACATCGCGGTGAGCGGACCAACCGCGACCG 1127
QY 187 LeuArgValGlyGluAlaLeuLeuGlyGluArgLeu----- 198
DB 1128 CTG-----GCCAGCGCGGTGATCGCGAGGCGCTGCGCAGCAGTGCAGCGCGCGCTCC 1181
QY 199 ProIleSerPheIleGlnAspVal-----ValIleValIleMetAlaLeuAlaPheLeu 215
DB 1182 CCGCGCGCGCTGAAAGAGGAGATCGACGCGCGGTGCGCGCGGTCTCCGCGAGGTGCTC 1241

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QY 216 AspValSerArgAsp-----AlaMetAlaLeuAspPro 226
DB 1242 GACACCGCGCGCGCATGACAGCAAGTCCGATCGCGCGCGCGCTCTCCGCG 1301
QY 227 ProAspPheIleThrGlyTyrGluPheValGluGluAlaLeuValLeuLeuGlnGlu 246
DB 1302 CAGGACAGCAGGTGCGG---GAGCTCATCGCGCGGATGACAGAGTGCAGAGGAC 1358
QY 247 GlyAlaSerSerLeuAlaProAspLeuArgAlaGlnIleAspGluThrLeuGlnGlu 265
DB 1359 GGTGTCAATCAACGTGAGAGATCCAACTTCGTGATGACCTGCACTTCAACGAGGC 1418
QY 266 -----IleThrProArgTyrValLeu-----GluLeuLeuGly 276
DB 1419 ATGCGCTTCGACAGGCGTACTGTCTCCCTGATCATGTGTGACCGACGAGAGGTATGAG 1478
QY 277 LeuProLeuGlyAspAspTyrAlaAlaIleValAsnGlyLeuSerGlyValArgAsn 296
DB 1479 GCGGTCTTCGACGACCGGTATCTGTATCCACGAGGAGAGATGTTGATTCAGAGAC 1538
QY 297 IleLeu----- 298
DB 1539 CTGCTGCGCGCTGTCGAGAGGTATCCAGGCGGTGCTCCAGCCGCTGCTGATCATC 1598
QY 299 ---TyrSerValGlyGlyGlyValAlaSerAlaLeuValGlyGlyLeuThrArgGly 317
DB 1599 GCCGAGACGTCGAGAGGCGAGGCGCTGTGACCTGTGTGTGTCACAAAGATCCGCGGACG 1658
QY 318 PheMetAsnGluAla-----PheLeuArgMetThrAlaAlaGluGluVal 332
DB 1659 TTCAAGCGCGTGCCTGTCAGAGCGCGCGCTTCGATGACCGCGGAGCGATGCTCGGC 1718
QY 333 AspLeuPheValAlaThrProSerAsnIleProAlaGluSerPheGluValTyrGluVal 352
DB 1719 GACATGCGCACCTTCACCGGTGTCACCGCTCATCGCGAG-----GAGGTC 1763
QY 353 AlaLeuAlaLeu-----ValAlaGluAlaPheIle 362
DB 1764 GCGCTCAAGCTGACAGCAGCGCGGTGTCAGCTGCGGACCGCGCGCGCTCACCTGTC 1823
QY 363 GlyIleValYsProHisLeuLeuGlnAlaAspIleAspGlnPheGlnGlnGlnAla 382
DB 1824 ACCAAGACGACAGACACCATGTGACCTGAGAGAGAGCGCGAGAGGTCCAGAGGC--- 1880
QY 383 LysValMetAlaMetGluIleProAlaMetLeuTyrAspThrArgAsnAsnTrpGluIle 402
DB 1881 -----CGGTGCGCCCATCAAGCGCGGATCGAGTCCGACTGCGAGCGCGC 1934
QY 403 AspPheGlyLeuGluArg-----GlyLeuCysAlaLeuLeuIleGly 416
DB 1935 GAGAGCTTCAGAGAGCGCTGCGCAAGTGCAGCGCGCGCGCTGTGATTCGCGTGGC 1994
QY 417 LysValAspGluCysArgMetTrpLeuGlyLeuAspSerGluAspSerGlnTyrArg--- 435
DB 1995 GCGGCCACCGAG-----GTCAAGCTGAGAGAGCGGACGAGACCGTCTG 2036
QY 436 -----AsnProAlaIleValGluPheValLeuGluAsnSerAsn 448
DB 2037 GAGAGCGCATTCGCGCAGACCGCGCGCGGTGAGAGGAGCATGTCTCCGCTGTGGC 2096
QY 449 Arg-----AspAsn-----AspAsp 454
DB 2097 TCCGCGCTGTCACGCGCGTCAAGGTCTGTGACGACCACTCGCGCGACCGCGCGAG 2156
QY 455 LeuProGlyLeuCysLysLeuLeuGluThr-----TrpLeuAla--- 467
DB 2157 GCCACCGGTGTGCGGTGTCTCGCGCGCGCGCGCGCGCGCTGATTCGCGAG 2216
QY 468 -----GlyValAlaPheProArgPheArgAspThrLysAspIleLysPhe 482
DB 2217 AACCGCGCTTCGAGGCTACGTATC-----ACCACCAAGATGCGCGAGGCTC 2264

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Qy 310 -----ValGlyGlyLeuThrArgGluYsPheMet----- 319
Db 1311 CGCTTGCTTGCGCATGAGACGAAAGAAAACGATGTTGATTCAGACGGCGCGCT 1370
Qy 320 -----AengLualApheLeuArgMetThrAlaGluGlnVal--AspLeuPheVa 336
Db 1371 CGCGCTAAATGGGAAAGAAATGCAACTGCTGCGCTGCGCTGCTGCTGCTGCTGCT 1430
Qy 336 LAlaThrProSerAenIleProAlaGluSer-----PheGluVa 349
Db 1431 GCGCGCTTAATCTGCTGATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1490
Qy 349 LTyGluValAlaLeuAlaLeuValAlaGlnAlaPheIleGlyLys--LysProHisLe 368
Db 1491 GCATCAGTACGAGCGCGTGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCG 1550
Qy 368 uLeuGlnAspAlaAspLysGlnPheGlnGlnLeu-----GlnGlnAlaLysValMetAl 386
Db 1551 GGTTCCTCATGAAACGACGCTTCCGACGACGCTGCTGCGCGCGCGCGCGCGCGCGCG 1610
Qy 386 AMecGluIleProAlaMetLeuTyPAspThrArgAspAsnTrpGlu--LleAspPheGl 405
Db 1611 GCTTAAAGAGCGCTTGATGAGACGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1670
Qy 405 YLeuGlnuArgGlyLeuCybAlaLeuLeuIleGly-----LysValAs 419
Db 1671 GCTGAAACACGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1730
Qy 419 pGluCybArgMet---TrpLeuGlyLeuAsp---SerGluAspSerGlnTyArgAspNr 437
Db 1731 CACGAGCGCGCTTGAAACAGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1779
Qy 437 oAlaIleValGluPheValLeuGlnuAsnSerAsnArgAspAsnAspAspLeuProGl 457
Db 1780 -GCGGTGACGCGCGCGCTTGACGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1836
Qy 457 YLeuCybLysLeuLeuGluThrTrpLeuAlaGlyValAlaPheProArgPheArgAspTh 477
Db 1837 -----AAACAGCTCGGAGCG-----GTTTATTGTCAGACGCTGACCTCCC 1877
Qy 477 rLysAspLysLysPheLysLeuGlyAspTyTrpAspAspProMetValLeuSerTyLe 497
Db 1878 GGTGTTGAAAAAGACAAAAACCGGC---TATTCCAGCTCAGCGCGATGCTAGAAAACT 1934
Qy 497 u---GluArgValGluValGlnGlySerProLeuAlaAlaAlaAlaThrMetAlaAr 516
Db 1935 TGACCGCGACCATGAAATCGTCGAA-----CATATTGTCATTAACCGCACTGCGCA 1988
Qy 516 gIleGlyValaGluHisValLysAlaSerAlaMetGlnAlaLeuGlnLysValPheProSe 536
Db 1989 GCTGACATCAACGTRATATTGA--GGGCTGCTGAAAGTGTGACACCCCGTACCGGCA 2045
Qy 536 rArgTyTrpAspArgAsnSerAlaGluProLysAspValGlnGluThr-----ValPh 554
Db 2046 AGTGACACACGATGTTCAATCAGCG-----TTGACGCAAAACCGGCGCGCTCAG 2093
Qy 554 eSerValAspProValGlyAsnAsnValGlyArgAspGlyGluProGlyValPheIleAl 574
Db 2094 CTCGCTGCAACCGAATTGCAAAACATTCGATTCGCTGAGAAAGGCGGAAATCGG 2153
Qy 574 aGluAlaValAlaArgProSerGlu-----AsnPheGluThrAs 586
Db 2154 CCAGCGCTTGCTGCTGCTGCGAGCGGACGCTGCTGCTGCGCGCGCGCGCGCGCGCG 2213
Qy 586 nAspTyTrpAlaIleArgAlaGlyLysSerGluSerValAspGluThrThrValGlu-- 605
Db 2214 CGACCTGCGCGCTGCTGCGCGCATATCGCGAA-----GATGCAATTTGATTGAAGC 2264
Qy 606 -----MetSerValAlaAspMetLeuLys 613
Db 2265 GTTCGCGCGCTGTTGACATCATCAACAAAAACGCGCATGCAATTTTCATGTCAGCGA 2324
Qy 613 sGlu-----AlaSerValLysIleLeuAlaIleGlyValAlaIleGlyLeuIleSe 630

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Db 2325 AGAAGACGTGACAGCAACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2384
Qy 630 rLeuPheSerGlnuTyTrpPheLeuLysSerSerSerSerPheGlnAlaGlyAspMetVa 650
Db 2385 CGGCATTTGATGAT---TACGGTCTGCGCGCAAACTTGAACATTAACCGCGCAAGCGCG 2441
Qy 650 lSerMetGluSerAspValAlaThrIleGlySerValArgAlaAspAspSerGluAl 670
Db 2442 TGCAATTTATGACCATATTGTCAGCTTTCCAGCTGTAAG----- 2484
Qy 670 aLeuProArgMetAspAlaArgThrAlaGluAsnIleValSerLysTyTrpGlnLysIle 690
Db 2485 -----CAATATATGACACAACTTGGCAAGAA--GCGAAACAAA 2522
Qy 690 sSerLeuAlaPheGlyProAspPheIleArgIleGluMetLeuProGluValLeuAspGlyAr 710
Db 2523 AGGGTATGTGACGACGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2582
Qy 710 gMet---LeuLysIleTyTrpThrAspArgAlaAla---GluThrAlaGlnLeuGlyLeuVa 728
Db 2583 CTTCAACGCTCGCGACGTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2642
Qy 728 lTyAspTyTrpThrLeuLeuLysLysSerValAsp---SerValThrValSerAlaAspGl 747
Db 2643 TGCCGAC---ATCATTAAGAAAGCATGATGATCTTAAGCGTGAAGCGCGCGCGCGCGCG 2699
Qy 747 YThrArgAla-----LeuValGluAlaThrLeuGl 757
Db 2700 GCTGACGCGCGCGCGCTGTTGCTGCAAGTCATGACGAACTCAATTTTGAGAGCGCG 2759
Qy 757 uGluSerAlaCybLysSerAspLeuValHisProGlu 769
Db 2760 GGAATTCGACGCGCTGCGCGCGCTGCTGTT---CCGAA 2793

RESULT 5
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A.
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 32.9 Length: 4411529
Score: 139.00 Matches: 206
Percent Similarity: 32.1% Conservative: 101
Best Local Similarity: 21.5% Mismatches: 328
Query Match: 3.4% Indels: 323
DB: 3 Gaps: 47

US-10-600-070B-2 (1-801) x US-09-103-840A-1 (1-4411529)

Qy 17 CybArgLeuProProAlaThrThrLysLeuArgArgSerHisAsnThrSerThrIle 36
Db 3401725 TGCCATTTGCGCGCGCGCGCTGACATCGCTGCTGCG-----GGGTGCGCTTGG 3401678
Qy 37 CybSerAlaSerLysTrpAlaAspArgLeuLeuSerAspPheAsnPheThrSerAspSer 56

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Db	3401677	TGCTCGGTAGAGCGGCTAGGCGGG-----TTGACGCTCGGAACCTGCTCGGTCG	3401624
Qy	57	SeSer-----SeSerPheAlaThrAlaThrThrAlaThrLeuVal	71
Db	3401623	GGCTCAGTCTCTCGCGGCTGCGGAGCGGGTCCCGGCGAGCAAGCGGTCCGCACTTGG	3401564
Qy	72	SeLeuProProSeSerIleAspArg-----ProGluArgHisValProIle--	86
Db	3401563	TCGTCTCGCGGGGTATCACTG--TTGGGCGGTGTGGCGCGGCTCTACGAGCGCTCGAC	3401505
Qy	87	-----ProIleAspPheTyrgLValLeuGlyAlaGlnThrHisPhe-----	100
Db	3401504	TACCAACCGCGCGATCGACATCTGTGAAGAGCCTGTGGCGCTGAG---CATTTGGCCAAACGC	3401448
Qy	101	-----LeuThrAspGlyLLeArg---ArgAlaPheGluAlaArg--ValSer	114
Db	3401447	ACATACGGAACACTGTCCGAGGGGCGAGCGCAAGAGCTGATTCGCGGGGCTTTATG	3401388
Qy	115	LysProProGlnPheGlyPheSerAspAspAla-----LeuIleSerArg	129
Db	3401387	ACAGATTCAGAGCTGTCTGTCTGTGACGAAACCGCGCGGCGCTGACTTACGTAGTGGCGA	3401328
Qy	130	ArgGlnIleLeuGlnAlaAlaCyseGlnThrLeuSerAsnProArgSerArgArgGlyTr	149
Db	3401327	GAGGAATGTGTGCGCCGCGCTGAGCGGACCTGTGGACCGCACCT-----	3401286
Qy	150	AsnGlnGlyLeuLeuAspAspGlnGlnAlaThrValIleThrAspValProTrpAspLys	169
Db	3401285	-----GACGCGCGCGCGTGTGTCTGTGTGACCCACCACTGAGAG	3401244
Qy	170	ValProGlyAlaLeu-----CysValLeuGlnGlnGlyGlyGlnThrGluIleValLeu	187
Db	3401243	ATTCCGCGCGGCTTCAAGCATTTGCTGTCTGTGTGAGAGCGCGGGTGTTCGCGCGGC	3401184
Qy	188	ArgValGlyGlnAlaLeuLeuArgGlnArgLeuProLysSerPheLysGlnAspValVal	207
Db	3401183	TTGCTTCCCGACGCGCTGACGCGCGAGAACTGTCTCAACCGGGTGTGGCGAAGATCAACG	3401124
Qy	208	LeuValMetAla-LeuAlaPheLeuAspValSerArgAspAlaMetAlaLeuAspProPr	227
Db	3401123	CTGAGAGGCGCGGACGCGGCG-----GATATTGTCCCGACGCGCGTGGACCGCGAGCACC	3401070
Qy	227	AspPheIleThrGlyTyrgLnPheValGlnGluAla-----LeuLysLeuLeuGlnG	245
Db	3401069	C---ATCGAGAGCACTCATGATTCACTCGGAGACCACTGTACCCCGGCTTACACCGA	3401013
Qy	245	GlnGlnAlaSerSerLeuAlaProAspLeuArgAlaGlnIleAspGlnThrLeuGlnG	265
Db	3401012	GCGCGGCGCGGCGAC-----CGTGA	3400995
Qy	265	uIleThrProArg-----TyrValLeuGlnLeuLeuGlyLeuPr	278
Db	3400994	TGTTGTGTCCGCGACCCGCGAGCGCGGATCAGCGTCCGCTGTGCGCGCTTCTTGATCGGC	3400935
Qy	278	LeuLeuLysAspAspTyrgLAlaAlaLysArgLeuAsnGlyLeuSer-----	292
Db	3400934	GGCACGCTGCGATGATTTCCGCGCGGGGTATGTGTCTTCCGCGCGGGGAGTCAACG	3400875
Qy	293	-----GlyValArgAsnIleLeuTrpSerValGlyGlyGly-----AlaSerAla	309
Db	3400874	ACCGGACCGCGACCCGCACTTGGGCGCGGTGTGGGGCAATGGCGCGGTCCGCGCGGAGT	3400815
Qy	309	uValGlyLeuThrArgGlnLysPheMetAsnGlnAlaPheLeuArgMet-ThrAla	329
Db	3400814	GGTGGGCGGAGCGGTTCCGCACTCAGCGCTGATCTGCGCGAAGCTTGTGTTCGCGCGGGG	3400755
Qy	329	IaGlnGln-----ValAspLeuPheVal	337
Db	3400754	CCCGGAGAGCGTTTCAGAGAGTCCGGGGTGTATTGCGCGCGCGGCTCATTCAGACCACTT	3400699
Qy	337	IaThrProSerAsnIleProAlaGlnSerPheGlnValTyrgLValAlaLeuAlaLeu	357

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Db      3400694 CGGCACCGGAACAGCATGCTCGAGAGCC--TCGGTGTACGGCGACGCGCGTCCGCGCAC 3400638
QY      357      alAlaGlnAla----- 360
Db      3400637 TGGCGCAACCGGACCGCTCTCTCGCGGACCTTCTCGACAGCGGAAAAAGCTGGTCTCGCAT 3400578
QY      360      ----- 360
Db      3400577 CGGACCTGTCTACGCGCCCTGGGGCCAACTGGGTTCACCCCGAGGCCGAACCTGACCCGGCGCT 3400518
QY      361      -----PheIIleGlyIlyblybProHis 367
Db      3400517 ACGACACCTTACTTCTTGTGGGTGTCCTTACTTGAAGGTCAAGCCGCGCGACGCGGAGAACCA 3400458
QY      368      -----LeuIleuGlnAapAlaApIlybGlnPhe----- 376
Db      3400457 CCGAATCCGACCGCGGCTGGTGGGTGTGGCAGCGCAGCGCTTACCGCACTTGCGCGCGG 3400398
QY      377      -----GlnGlnIleuGlnGln----- 381
Db      3400397 GCGGCAACTTCTTGCTGCTCGCGCGACCTGACGCAAGCAACTGACTCGTGGCGGTATACCG 3400338
QY      382      --AlaIlybValMeAlaMeGln-----IleProAlaMeIleuTyIAspThrArg 398
Db      3400337 TTGCGCAGCTGTGCGCTGCTGCAACGCGCAATTCGTCGGGTGACACCACTGCGCGCGCA 3400278
QY      398      An-----AsnTrpGlnIleAsp-----PheGlyIleuGlnIaIrgIlyLeuCyAlaIleuLeuI 415
Db      3400277 ACGCGCAACAATCTGGAGATGCAAGTCTTCATTCGACCGCTTAAACAGGCCCGGAG-A 3400219
QY      415      IeGlyIyValaIAspGlnCyAspIgneTrIleuGlyLeuAspSerGlnAspSerGlnTyra 435
Db      3400218 TCGGCGCGATCGACCGGGGTGCGCGCT-----G 3400192
QY      435      rgaAsnProAlaIleValaGlnPheValaIleuGlnuAsnSerAAspAspAsnAspAsp 455
Db      3400191 TGACGCCAACGCTGCGCGAGTTCGTC-----AACGTGCTGTACGTACGGCTCCAGG 3400138
QY      455      euProGlyIleuCyblybIleuLeu----- 462
Db      3400137 ATGCGCGGCTGGCCATGTTGTTCTCTATGCGACCGCTACCAACGCGATGACCGCGCAG 3400078
QY      462      ----- 462
Db      3400077 TCTACCGGGAAGTGGTCGCGCGCGCAACGAGCTGGGCGACCGGACGACGCTGGCGCAG 3400018
QY      463      -----GlnThrTrpIleuAlaGlyValaIValaPheProArgPheArg- 475
Db      3400017 TGATCTGTATGCGCGCGCACCAAAATCTTCTCCGCGCGCGACGACATCCCGAACTGGCGA 3399958
QY      476      -----AspThrIyAspIlybIyAspIlybPheIyIyAspIyTyIAspAspProm 492
Db      3399957 CATTGACGCGCGCAGAGGCGCAACGCCGCGCGGATTCGCGACAGGCGCGTGAACCGCG 3398988
QY      492      etValaIleuSerTyIleuGlnIyAspValaGlnValaIValaGlnGlySerProIleuAlaIla 512
Db      3398987 TTGCGCGCATCCCAAGCCGACGCGCGCTGGCGCGCATCAACCGGATACGCGTGGGTGCGCGCC 3398388
QY      512      IaThrMeAla-----ArgIIleGlyAlaGlnIleValaIlyAlaIAspSerIam 527
Db      3398387 TTACGCTGGCCCTTACCGCGCGCATGCGCGATGCGAGTCAACGCGGTACAACTGAATTCGGCGCGA 3399788
QY      527      etGlnAlaIleuGlnIyValaPheProSer-----ArgTyIThrAspArg 542
Db      3399777 CCGAAGTCTGTGCGCGCGCTGATCCCAAGCGCGCGCAAGCAATGGCCGCGTGACG-----C 3399724
QY      542      snSerAlaGlnIyProIyAspAspValaGlnIyIthrValaPheSerValaAspProValaIyAsn 562
Db      3399723 GAGCGCGCGGTCTCGACGACGACGACGAGAGGTGTTCACG----- 3399683
QY      562      snValaGlyArg-----AspGlyIyIyProGlyVala-----PheIleAlaGlnIyIaV 577
Db      3399682 -----GGGGGCTTCTTTCAGACGCGGAGAGGCGCTTGGCGCTGGCGCTGTGATTCAGACGACATGG 3399628

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Qy 577 a1ArgProSerGluAnpHeGluThrAsnAsp-----587
Db 3399627 TGGCCCCGACGACGTTTACGACGCCGCGCGCTGGGCGAGCGCTTTTACGCGCC 3399568
Qy 588 -----TyrAlaIleArgAlaGlyValSerGluSerSerValAspGluThrT 603
Db 3399567 CGCCGACGCGCTGGCCCGCGCAAGCGCGGATCAGCGAC-----G 3399526
Qy 603 hrValGluMetSerValAlaAspMetLeuLysGlu-----614
Db 3399525 TCTACGACCTGGCCGCGCGCGGATCGCGCTGAGCGTGGCGCTTATGTCAGGCTGT 3399466
Qy 615 --AlaSer-ValLysIleLeuAlaIleValAlaIleGlyLeuIleSerLeuPheSer 633
Db 3399465 TCGCGCTGCTCAAGCTGTGTGCGACGAGCGGCGCGCGCTTACGCTC-----3399412
Qy 634 GluLysTyrPheLeuLysSerSerSerSerPheGluThrGlyAspMetValSerSerMet 653
Db 3399411 --GCTATATGACGAGGATTCAAACATC-----CCGCGCAGCGCACTCCCAATCCA 3399361
Qy 654 GluSerAspValAlaThrIleGlySerValArgAlaAspAspSerGluAlaLeuProArg 673
Db 3399360 CATGCGACGCGCGGACGAGCTGCGCGCTGCGCAGCAGCAAGCTGCGCGAGTGTCTC 3399301
Qy 674 MetAspAlaArgThrAlaGluAsnIleValSerLysTyr-----GluLys 688
Db 3399300 TACGACGACTGGGAAGCGGAAATACGACGAGAGTGTGTCTTATGACCAAGCTGT 3399241
Qy 689 IleLysSerLeuAlaPheGly-----ProAspIleArgIleGluMet 702
Db 3399240 TGCCTGCACTACGCGCGCGCGCTTCAAGCATGCTGCTGATGAGTGTATCGCGCAG 3399181
Qy 703 LeuProGluValLeuAspGlyArgMetLeuLysIleThrThrAspArgAlaAlaGluThr 722
Db 3399180 CTGGCC-----TACGACCGCGCACTGGAA---3399157
Qy 723 AlaGluIleGlyLeuValTyrAspTyrThrLeuLeuLysLeu 736
Db 3399156 -----CTGGGCTGTGGAAACCGGATTCCTCTGCTCAACTTG 3399121

RESULT 6
US-08-436-664-33
; Sequence 33, Application US/08436664
; Patent No. 5874282
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATTHEW
; APPLICANT: TUDOR, STARLA D.
; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
; TITLE OF INVENTION: STEAROTHERMOPHILUS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,664
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/394,232
; FILING DATE:
; APPLICATION NUMBER: 08/307,410
; FILING DATE: 16-SEP-1994

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; APPLICATION NUMBER: 08/222,612
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94003.CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2631
; OTHER INFORMATION:
; US-08-436-664-33

Alignment Scores:
Pred. No.: 0.000192 Length: 2631
Score: 136.50 Matches: 191
Percent Similarity: 37.2% Conservative: 143
Best Local Similarity: 21.3% Mismatches: 364
Query Match: 3.4% Indels: 200
DB: 2 Gaps: 44

US-10-600-070B-2 (1-801) x US-08-436-664-33 (1-2631)
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Db 47 GCGCTTTTTCGCTGCGCTTTTTCATACGATTAAGGATTCATACGACGATCT 106
Qy 32 ThrSerThrThrIleCySerAlaSerLysIleAlaAspArgLeuLeuSerAspPheAsn 51
Db 107 ACGGTTTACGATGATGTTAAACAAATTTGGGGAAGACACCGACCAATTCG 166
Qy 52 PheThrSerAspSerSerSerSerPheAlaThr-----ThrThra 68
Db 167 TGGCGTTT-GACGCGCGGGAACGACGTTCCGCATGAAACGTTCCAAAGCGGAAGGC 225
Qy 69 ThrLeuValSerLeuProProSerIleAspArgProGluArgHisValProIleProIle 68
Db 226 GCGCGGACGACGACGCGCGGAACGTGCGGACGATTCGCTGCGCGGAATTCGTC 285
Qy 89 AspPheTyrGluValLeuGlyAlaGln---ThrHisPheLeuThrAspGlyIleArgArg 107
Db 286 AAGCGTACCGCATCCCGCTAGACTGACCATTAACGAGCGACGATTTATCGGA 345
Qy 108 AlaPheGluValArgValSerLysProProGluIlePheSerAspAspAlaLeuIle 127
Db 346 ACGATGCGGCGCGCGGTGACGAGAA-----GGGTTGACGAGAAAGTCATTTC 396
Qy 128 SerArgArgGlnIleLeuGlnAlaIleCysGluThrLeuSerAsnProArgSerArgArg 147
Db 397 GCGACCGCGATTTAACCG-----CTTGGTTCCCGCAAGTACGCGTG 441
Qy 148 GluTyr---AsnGluGlyLeuLeuAspAspGluGluAlaThrValIleThrAspVal--- 165
Db 442 GAGATTACGAAAAAGGATTTACGACATGATGTCACACGCGGAGACGCTGTGGA 501
Qy 166 -----ProTyr 167
Db 502 AATACGCGCTCACCCGCGAGCAAAATTGTGCACTTGAAGGATGTGCGGCAAAATCC 561

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Oy	168	AapbyvalProgly-----	AlaLeuCyValLeuGlnGlu	179
Db	562	GACAAACATCCCTGGCGCGCCCGGATGGGAAAAAACAGCCGTCAAGCTCTCAAGCAA	621	
Oy	180	GlyGlyGluThrGluIleValLeuArgValGlyGluAlaLeuLeuGlySerGluThrGluPro	199	
Db	622	TTCCGCACCGGTCAAAACGTACTGGCATCGATGATGATCAAAAGGAGAAAGCTGAAA	681	
Oy	200	LysSerPheLeuSerGln-----	AspValIleValMetAlaLeuAlaPheLeuAspVal	217
Db	682	GAATAATTTGGCCCAATATCCGGGATTTTGGCGTT-----	TTAAGCAAAACAGCTGGCGCATTT	738
Oy	218	SerArgAspAla-----	MetAlaLeuAspProPheAspPheIleThrGlyTyrGlu	234
Db	739	TGCCCGCAGCGCCCGGTTGAGCTGACCTCGAT-----	GACATTGCTCTCAAAAGAGAA	792
Oy	235	PheValGluGluAlaLeuLysLeuLeuGlnGluGluLysIleSerLeuAlaProAsp	254	
Db	793	GACCGGAAAAAAGTGCTGCGCTTTTTCAGAGCTCGAATTCAGTCTTTTCGACAG	852	
Oy	255	LeuArgAlaGlnIleAspGlu-----	ThrLeu	263
Db	853	ATGGCCGCTTCAACCGATGAAAGCGCAAAAGCCGCTCCCGCGGAGATTTTGGCATGCC	912	
Oy	264	GluGluIleThrProArgTyrValLeuGluLeuLeuGlyLeu-----	ProLeuGly	280
Db	913	GACAGCGTCACGGACGAATAGCTCGCCGACAAAGCGGCCCTCTCGTGAAGTGGTGGGC	972	
Oy	281	AspAspTyrAlaAlaLysArgGluAsnGlyLeuSerGlyValArgAsnIleLeuTrpSe	300	
Db	973	GACAACTATCACCATGCCCCCATGTTCTGGAGTCCGCT-----	TGGCC	1014
Oy	300	ValGlyGlyGlyGlyLysIleAspAlaLeuValGlyGlyLeuThrArgGluLysPheMet	320	
Db	1015	AACGACCGCGGCGGTTTCTCTGCGCCCGGAGACGGCGCTCGCGCATCCGAATTTCTC	1074	
Oy	320	snGluAlaPhe-----		323
Db	1075	GCTTGCGCTTGGCGATGACGAAAGAAAAACGATTTTGATTCAAACCGGCGCGCGTC	1134	
Oy	324	-----	LeuArgMetThrAlaAlaGluGlnValAspLeuPheValAlaThr	338
Db	1135	GCGCTAAATGGAAAGAAATGCAATCGACGCGCGCGTCTGATCTTTCTGTGGCGCT	1194	
Oy	339	ProSerAsnIleProAlaGluSer-----	PheGluValTyrGlu	351
Db	1195	TACTTGCTCGATTCGGCGGACGGCGGCGGCGACGTTGGCGCGTGCGAAATGATCATAG	1254	
Oy	352	ValAlaLeuAlaLeuValAlaGlnAlaPheIleGlyLys-----		364
Db	1255	TACGAGCGCGTCCGATCCGATGAGCGCGTCTATGAAAAAGACGACGACCGAGTCTCT	1314	
Oy	365	---LysPheIleLeuLeuGlnAspAlaSerLysGlnPheGlnIleLeuGlnAlaLys	383	
Db	1315	GATGAACCCACGCTTGCCGACGATCTCGCCGCC-----	AAGCGCGCGCC	1359
Oy	384	ValMetAlaMetGlnIleProAlaMetLeuTyrAspThrArgAsnAsnTrpGlu---Ile	402	
Db	1360	ATTTGCGCGCTTGAAAGCGCTTGATGAGCAAGATCGCCGACAGCAAGATGCGCTG	1419	
Oy	403	AspPheGlyLeuGlnArgGlyLeuCyValAlaLeuIleIleGly-----		416
Db	1420	CTGACCGAGCTCGAACCGCGCTGGCTGGCATTTTGGCCAAATATGGAATTTACTGAGAGT	1479	
Oy	417	LysValAspGluCysArgMet---TrpLeuGlyLeuAsp---SerGluAspSerGlnTyr	434	
Db	1480	AAATGGACACGAAGCGGCTTGAAACAGATGGGGCGGAGACTCAGACGACGTGCAG---	1533	
Oy	435	ArgAsnProAlaIleValGluPheValLeuGluAsnSerAsnArgAspAsnAspAsp	454	
Db	1537	-----CGGATCGAGCGGCGCATTTACGAATCGCGCGGCAAGAGTTTCAACATTAC	1587	
Oy	455	LeuProGlyLeuCyValLeuLeuGlnGluThrTrpLeuAlaGlyValValaPheProArgPhe	474	

Db 1588 TCGCC-----AAACGCTCGGGACG-----GTTTATTTCACACGCTG 1626
 Qy 475 ArgAspThrIlyAspIlySerPheIlySerLeuGlyAspTyrTyrAspAspProMetValLeu 494
 Db 1627 CAGCTCCCGGCTGTTGAAAAAGCAAAACCGCG--TATTGCAGTTCACCGCATGTGCTT 1683
 Qy 495 SerTyrIleu---GluArgValGluValValGlnGlySerProLeuAlaIalaIalaThr 513
 Db 1684 GAGAACTTCACCGCACCATGCAAAATCGTCGAA-----CATATTTTGCAATACCGCCAA 1737
 Qy 514 MetAlaArgTleGlyAlaGluHisValIlyValAspSerAlaMetGlnAlaLeuGlnIlyVal 533
 Db 1738 CTGGCAAGGTGAGTCACACGATATTGAA--GGGCTGCTGAAGATGGTGCACCCCGG 1794
 Qy 534 PheProSerArgTyrThrAspArgAsnSerAlaGluProIlyAspValGlnGluThr--- 552
 Db 1795 ACGGGCAAAAGTCACACGATGTTCAATCAGCGG-----TTGACGCAAAACCGGG 1842
 Qy 553 ---ValPheSerValaAspProValGlyAsnAsnValGlyArgAspIlyGluProGlyVal 571
 Db 1843 CGCTCAGCTCCGTCGAAACCGAATTTGCAAAACATTCCGATTCGCTTGAGGAAGGGCGG 1902
 Qy 572 PheIleAlaGluAlaValArgProSerGlu-----AspPhe 583
 Db 1903 AAAATTCGCGCAAGGGGTTCGTCGCTGCGACCGGACTGCTACTTTGCGCGGCATCT 1962
 Qy 584 GluThrAsnAspTyrAlaIleArgAlaGlyValSerGlnSerSerValaAspGluThrThr 603
 Db 1963 TCGCAATTCAGCTCGCGCGCTCTCGCCCATATCGCGGA-----CATGCAATTTGG 2013
 Qy 604 ValGlu-----MetSerValaIaAsp 610
 Db 2014 ATTGAAGGTCCTCCGCGCGGTGGACATCCATACGAAACAGCCATGAGCATTTTTCAT 2073
 Qy 611 MetLeuAspGlu-----AlaSerValIlyIleLeuAlaIleGlyValaIleGly 627
 Db 2074 GTGAGCGCAAGAAAGCTGACAGCCACACATGCGCGCCAGCAGGCGGCTCATTTTGCG 2133
 Qy 628 LeuIleSerLeuPheSerGlnIlyTyrPheIlySerSerSerSerPheGlnArgIlyS 647
 Db 2134 ATCGGTACGGCATTTAGTAT--TACGCTGCGCGCAAAACTGACATTTAGCGCGCAA 2190
 Qy 648 AspMetValSerSerMetGluSerAspValAlaThrIleGlySerValaArgAlaAspAsp 667
 Db 2191 GAAGCGCTGATTTATTGACCGATATTTTGGCCGTTTCCAGGTGTAAAG----- 2241
 Qy 668 SerGluAlaLeuProArgMetAspAlaArgThrAlaGluSerIleValSerIlyTyrGln 687
 Db 2242 -----CAATATATGACAAACATTTGTGCAAGAA---GCG 2271
 Qy 688 IlyIleIlySerLeuAlaPheGlyProAspHisArgIleGluMetLeuProGluValLeu 707
 Db 2272 AAACAAAAAGGTATGATGACAGCGCTGTCATCGCGCGCTATTGTCGCGATATTA 2331
 Qy 708 AspGlyArgMet---LeuIlyIleTyrThrAspArgAlaIa---GluThrAlaGlnLeu 725
 Db 2332 AGCCGCAACTTCAGAGTCGCGCGACTTCGCCAGCGGAGACGGGATGAACACCGCATCCA 2391
 Qy 726 GlyLeuValTyrAspTyrThrLeuIlySerValaAsp---SerValThrValSer 744
 Db 2392 GGGAGTGCCTGTAT--ATTATTAATAAAGCATGATGATCTTAAGGTGAGGCTGGC 2448
 Qy 745 AlaAspGlyThrArgAla-----LeuValGluAla 754
 Db 2449 GAAGAAAGCGCTGACAGCGCGCTGTGTCGCAAGTGACATGACGAATCATTTTGAGCGC 2508
 Qy 755 ThrLeuGluIlySerAlaCylSerSerAspLeuValHisProGlu 769
 Db 2509 CCGAAAGAGAAATCGAGCGCGCTGTGCGGCTTCGTT---CCAGAG 2550

RESULT 7
 US-09-135-642-33

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: Sequence 33, Application US/09135642
: Patent No. 6066483
: GENERAL INFORMATION:
: APPLICANT: RIGGS, MICHAEL G.
: APPLICANT: SIVARAM, MATHOOR
: APPLICANT: TUDOR, STARLA D.
: TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
: TITLE OF INVENTION: STEAROTHERMOPHILUS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Gen-Probe Incorporated
: STREET: 9880 Campus Point Drive
: CITY: San Diego
: STATE: CA
: COUNTRY: USA
: ZIP: 92121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/135,642
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/394,232
: FILING DATE:
: APPLICATION NUMBER: 08/307,410
: FILING DATE: 16-SEP-1994
: APPLICATION NUMBER: 08/222,612
: FILING DATE: 16-SEP-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Fisher, Carlos A
: REGISTRATION NUMBER: 36,510
: REFERENCE/DOCKET NUMBER: GP94003.CP2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-535-2807
: TELEFAX: 619-546-7929
: TELEX:
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2631 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 1..2631
: OTHER INFORMATION:
: US-09-135-642-33
:
: Alignment Scores:
: Pred. No.: 0.000192 Length: 2631
: Score: 136.50 Matches: 191
: Percent Similarity: 37.2% Conservative: 143
: Best Local Similarity: 21.3% Mismatches: 364
: Query Match: 3.4% Indels: 200
: DB: 3 Gaps: 44
:
: US-10-600-070B-2 (1-801) x US-09-135-642-33 (1-2631)
:
: Oy 12 SerProPheGlnLeuCyAlaArgLeuProProAlaThrThrIleuLeuArgArgSerHisAsn 31
: Db 47 GCGCGCTTTTCGCGTGGCCGTTTTCATTAACGATTAAGGAGTTTCATACGAACGCGAGTCT 106
: Oy 32 ThrSerThrThrIleCysSerAlaSerIleSTPAlaAspArgLeuLeuSerIlePheAsn 51

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Db	107	ACGGGTTTACAGTGAATGTTAAACAAATTTTGGCGGAAGACGACCGACCATTCCTGC	166
Qy	52	PhehrnSerAepSerSerSerSerSerPheAlaThrAlaThr-----ThrThrAla	68
Db	167	TGGCGCTTT-GACGGCGGGAAAAAGCAGCTTCGCCCATGAAGCTTCCAGACGGCAAGGC	225
Qy	69	ThrlleuValSerLeuProProSerIleAbaPargProGluArgHisValProIleProIle	88
Db	226	GGCGGCGACAGACGCCCGCGGAACTGTCGGAACAGTTTCCGCTGTCGGCAATTGCTC	285
Qy	89	AepPheTyrglnValIleuGlnIalValagln---ThrlIaphleuThrArgPlyIleArgArg	107
Db	286	AAAGGCTACCGCATCCCGCGCTATAGACTCGACCATTAACGAAGCGGACCATATTACGCA	345
Qy	108	AlaPheGluAlaArgValSerIleProProGlnPheGlyPheSerAbaPalaLeuIle	127
Db	346	ACGATGCGCGCGCGGCTGACGGAAGAA-----GGGTTTGACATGAAGTCATTTC	396
Qy	128	SerArgArgGlnIleuGlnIalAlaCysoGluThrIleSerAbaProArgSerArgArg	147
Db	397	GCGGACCGCGATTTAACCCAG-----CTTGCTTCCCGGAACTGACGCGTG	441
Qy	148	GluTyrgln---AeuglnGlyLeuLeuAbaPbaPbaGluGluAlaThrValIlePheAbaPala	165
Db	442	GAGATTACGAAAAAAGGATTCACGACATCGAGTGTACGCGCGGAGACGGTCGTGCA	501
Qy	166	-----ProTyr	167
Db	502	AAATACGGCTCACCCCGGAGCAATTCGACTTGCAAGATTAAGTATGGCGGACAAATCC	561
Qy	168	AbaPlyBValProGly-----AlaLeuCyValIleuGlnGlu-179	
Db	562	GACACACATCCCTGGGCGTCCCGGCATCGGGGAAAAACAGCGCTGACGCTGTCAAGCA	621
Qy	180	GlyGlyGluThrGlnIleValIleuArgValGlyGlyAlaIleuLeuTyIleGluArgPro	199
Db	622	TTCCGACACGCTCGAAAAAGTACTGCGCATCGATCAATGAGATMAAGGAGAAAGCTGAAA	681
Qy	200	LysSerPheIysGln-----AbaPalaValIleuValMetAlaLeuAlaPheLeuAbaPala	217
Db	682	GAATATTGGCCCAATACCGGAGATTGGCGCTT---TTAAGCAACAGCTGCGCGTATT	738
Qy	218	SerArgAbaPala-----MetAlaLeuAbaPbaProPbaPheIleThrGlyTyrglu	234
Db	739	TGCCGCGACGCGCCCGGTGACCTGACGCTGCAT-----GACATTGTCTACAAAGAGAA	792
Qy	235	PheValGluGluAlaIleuLeuLeuGlnGlnGluGluIalaserSerLeuAlaProAba	254
Db	793	GACCGGGAAAAAGTGTGTGCCCTGTTTCAAGAGCTCGAGATTCAGTCTGTTCTCGACAAG	852
Qy	255	LeuArgAlaGlnIleAbaPala-----ThrLeu	263
Db	853	ATGGCCCGTCCAAAGCATGAAAGGCGAAAAAGCCGTCGCCCGGATGATTTTGCATCGC	912
Qy	264	GluGluIleThrProArgTyrglnValIleuGluLeuGlnGlyLeu-----ProLeuGly	280
Db	913	GACAGCGCTACGAGCAAAATCTCGCCGACAAAGCGGCTCTGTCGAGAGTGTGGGC	972
Qy	281	AbaPbaPheTyrglnAlaIalArgIleuAbaGlyLeuSerGlyValArgAbaIleuIleuTyr	300
Db	973	GACACATATACCATGCCCCGATGTGTGGGATCGCT-----TGCC	1014
Qy	300	rValGlyGlyGlyIalaser-AlaLeuValGlyGlyLeuThrArgGluIysPheMetA	320
Db	1015	AAAGCAAGCGGGGGGTTTTTCTCGCGCCGAGACGGGCGTCTGCCGATCCGAAATTTCTC	1074
Qy	320	bnGluAlaPhe-----	323
Db	1075	GCTTGCTGTGGCGATGACAGAAAGAAAAACGATGTTTGATTCAAAAGCGGCGCGCTTC	1133
Qy	324	-----LeuArgMetThrAlaIalGluGlnVal-AbaPhePheValAlaThr	338
Db	1135	GCGCCTAAATGAAAGAAATGAACTGCGCGCGCTCGTGTTCATCTGTGTCGGCGCT	1194


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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...2631
OTHER INFORMATION:
US-08-394-232A-33

Alignment Scores:
Pred. No.: 0.000192 Length: 2631
Score: 136.50 Matches: 191
Percent Similarity: 37.2% Conservative: 143
Best Local Similarity: 21.3% Mismatches: 364
Query Match: 3.4% Indels: 200
DB: 3 Gaps: 44

US-10-600-070B-2 (1-801) x US-08-394-232A-33 (1-2631)

QY 12 SerProheGlnLeuCybArgLeuProProAlaThrThyLeuLeuArgSerHisIaan 31
DB 47 GGGCTTTTCCGCTTGGCTTTTGCATACGATTAAGGATTTCATACGACGCGCT 106
QY 32 ThrSerThrThrLeuCySerAlaSerLysTrpAlaAspArgLeuLeuSerAspPhean 51
DB 107 ACGGTTTACGATGATTAAACAAATTTGGCGGAAGACGCCGACCCACATTTCTG 166
QY 52 PheThrSerAspSerSerSerSerPheAlaThr-----ThrThrala 68
DB 167 TGGCGTTT-GACGCGGGAACGACGTTCCGCGATGAACCGTTCCAGACGGAAGGC 225
QY 69 ThrLeuValSerLeuProProSerLLeaAspArgProGluArgHisValProIleProle 88
DB 226 GGGCGGACGACAGCCCGCGGACCTGCGAACGTTTCCGCTGCGCGCAATTGCTC 285
QY 89 AspPheTyrglnValLeuGlyValaGln---ThrHisPheLeuThrAspGlyLLeaArg 107
DB 286 AAGCGTACCGCATCCCGCTATAGCTCGACCATTCAGAACGCGACATTTATCGGA 345
QY 108 AlaPheGluAlaArgValSerLysProProGlnPheGlyPheSerAspAspAlaLeuIle 127
DB 346 ACGATGCGGCGCGGCTGACGAGAA-----GGTTTGCAGTGAAGTCATTTC 396
QY 128 SerArgArgGlnIleLeuGlnAlaAlaCybGluThrLeuSerAspProArgSerArg 147
DB 397 GCGGACCGCGATTAAACGAG-----CTTGCTTCCCGGACGTGACGCTG 441
QY 148 GluTyrr---AenGluGlyLeuLeuAspAspGluGluAlaThrValIleThrAspVal--- 165
DB 442 GAGATTACGAAAAAGGAGATTACGACATCGAGTCAACGCCGAGACGGTCTGGA 501
QY 166 -----ProTrrp 167
DB 502 AAATACGGCTCAACCCCGAGAAATTGTCACTTGAAGATTATGGCGACAAATCC 561
QY 168 AspLysValProGly-----AlaLeuCybValLeuGlnIu 179
DB 562 GACAAACATCCCTGGGCTGCCGCGATCGGGGAAAAACAGCGCTCACTGCTCAAGCA 621
QY 180 GlyGlyGluThrGlnIleValLeuArgValGlyGluAlaLeuLeuGlyGluArgLeuPro 199
DB 622 TTGGGACCGGTGAAACGTACTGCGATCGATCGATCAAGGAGAAAGCTGAA 681
QY 200 LysSerPheLysGln-----AspValValLeuValMetAlaLeuAlaPheLeuAspVal 217
DB 682 GAAATTTTGGCCCAATACCGGATTTGGCGCTT---TTAAGCAACACACTGGCGCTATT 738
QY 218 SerArgAspAla-----MetAlaLeuAspProProAspPheIleThrGlyTyrglu 234
DB 739 TGCGGCGACGCGCGGTTGAGCTGACGCTCAT-----GACATTGTCTCAAGAGAGA 792

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QY 235 PheValGluGluAlaLeuLysLeuLeuGlnGluGluGlyValaSerSerLeuAlaProAsp 254
DB 793 GACCGGAAAAAATGTCGCTGCTTTTTCAGAGACTCGAATTCAGTCTTTCGACAG 852
QY 255 LeuArgAlaGlnIleAspGlu-----ThrLeu 263
DB 853 ATGCGGCTCCAAACGATGAAGCGAAAGCCGCTGCGCGGATGATTTGGCATGCC 912
QY 264 GluGluIleThrProArgTyrgValLeuGluLeuGlyLeu-----ProLeuGly 280
DB 913 GACAGGTCAGGACGAAATGCTCGCCGACAAAGCGGCTCGTGTGAGTGTGCGG 972
QY 281 AspAspTyrr-AlaAlaLysArgLeuAsnGlyLeuSerGlyValArgAsnIleLeuTrpSe 300
DB 973 GACACTATACCATGCCCGCATTTGCGGATCGCT-----TGGCC 1014
QY 300 rValGlyGlyGlyAlaSer-AlaLeuValGlyGlyLeuThrArgGluLysPheMet 320
DB 1015 AACGAAACGGGCGGTTTTTCTGCGCGCGAGAGCGGCGCTCGCATCCGAAATTTCTC 1074
QY 320 snGluAlaPhe----- 323
DB 1075 GCTTGCTTGGGATGACGACGAAAGAAAGATTTGATTCAAGCGGCGCGCTC 1134
QY 324 -----LeuArgMetThrAlaAlaGluGlnVal-AspLeuPheValAlaThr 338
DB 1135 GCGCTTAAATGGAAGAAATCGAATCGCGCGCTGTGTGATGCTTGTGCGCGCT 1194
QY 339 ProSerAsnIleProAlaGluSer-----PheGluValTyrglu 351
DB 1195 TACTTGCTGATTCGCGCGGAGCGCGGCGACGTTGCCGCGTGGCAAAATGCTACG 1254
QY 352 ValAlaLeuAlaLeuValAlaGlnAlaPheIleGlyLys----- 364
DB 1255 TACGAGCGCGCTCGATTCGATGAGCGGCTGTGGAAGAAAGACGAAAGCGACGCTTCT 1314
QY 365 ---LysProHisLeuLeuGlnAspAlaAspLysGlnPheGlnGlnLeuGlnAlaLys 383
DB 1315 GATGAACCGACGCTTGGCGGACGATCTCGCGCC-----AAGCGCGGCGCC 1359
QY 384 ValMetAlaMetGluIleProAlaMetLeuTyrrAspThrArgAsnAsnTrpGlu---Ile 402
DB 1360 ATTGGGCGCTTGAAGACCGCTTGAAGACGAACTGCCCGGACAAACAAACAGATGGCTG 1419
QY 403 AspPheGlyLeuGluArgGlyLeuCybAlaLeuLeuIleGly----- 416
DB 1420 CTGACCGAGCTCGAAACCGCTGCTGCTGATTTGGCAATATGAAATTACTGAGTG 1479
QY 417 LysValAspGluCybArgMet---TrpLeuGlyLeuAsp---SerGluAspSerGlnTyrr 434
DB 1480 AAGGTGACACGAAACGCGCTTGAACAGATGGGCGGAGCTCAACGACACGCTGAG--- 1536
QY 435 ArgAsnProAlaIleValGluPheValLeuGluAsnSerAsnArgAspAspAspAsp 454
DB 1537 -----GCGGTGACGCGCGCATTTACAACTCGCGCGCAAGTTCAACATTAAAC 1587
QY 455 LeuProGlyLeuCybLysLeuLeuGlnIleThrTrpLeuAlaGlyValAlaPheProArgPhe 474
DB 1588 TCGCGG-----AAACAGCTCGGAGCG-----GTTTATTGTGACAAAGCTG 1626
QY 475 ArgAspThrLysAspLysLysPheLysLeuGlnLysAspTyrrTrpAspAspProMetValLeu 494
DB 1627 CAGCTCCGCTGTGAAACAAACAAACCGGCG---TTTTCGACTTTCGCGATGTGCTT 1683
QY 495 SerTyrrLeu---GluArgValGluValGlnGlySerProLeuAlaAlaAlaIleThr 513
DB 1684 GAGAACTTGCACCGCACCATGAATGCTGAA-----CATATTTCGATTACCGCCA 1737
QY 514 MetAlaArgIleGlyAlaGluHisValLysValaSerAlaMetGlnAlaLeuGlnLysVal 533
DB 1738 CTCGCAAGCTGCACTCAACGTATATTGAA---GCGGCTGTAAGAAAGTGTACACCGCTG 1794
QY 534 PheProSerArgTyrrThrAspArgAsnSerAlaGluProLysAspValGlnGluThr--- 552

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1795 ACCGGGCAAAATGCAACAGATGTTCAATCAGCGC-----TTGAGCGCAAAACCGGG 1842
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553 ----ValPheSerValAaPProValIGlyAaAaAaValGlyArgAaPglyProGlyVal 571
      ::|||::|||::|||
1843 CGCCTCAGCTCCGTCGAACCGAAATTTGCCAAABAACATTCGATTCGCTTGAGGAAGGCGG 1902
      ::|||::|||::|||
572 PheIleAaGluAaValArgProSerGlu-----AaPhe 583
      |||::|||::|||
1903 AAAATTCGCGCCAGGGGTTGTCGTCGCGCGAGCGCGAAGCTGCATCTTTGCCGCGCACTAT 1962
      |||::|||::|||
584 GluThrAaAaPtyrAlaIleArgAlaGlyValSerGluSerSerValAaPglyThr 603
      ::|||::|||::|||
1963 TCGCAATCATGAGCTGCGGCTCTCGCCCATATCGCGAA-----GATGACAAATTTG 2013
      ::|||::|||::|||
604 ValGlu-----MetSerValAlaAaP 610
      ::|||::|||::|||
2014 ATTGAAGCGCTTCGGCGCGCGCTTGAGCATTCATAAGAAAACAGCATGACATTTTCAT 2073
      ::|||::|||::|||
611 MetLeuLyGlu-----AaSerValLySileuAlaAlaGlyValAlaIleGly 627
      ::|||::|||::|||
2074 GTGAGCGAAGAAGACGTGACACGCAACAGCGCGCCAGACGAAGCGCTCAATTTGGC 2133
      ::|||::|||::|||
628 LeuIleSerLeuPheSerGluLySlyrPheLeuLySerSerSerSerPheGluArgLyS 647
      ::|||::|||::|||
2134 ATCGTGTACGGCATTTGTGAT--TACGCTCTCGCCAAACATTTGAACATTAACGCGCAAA 2190
      ::|||::|||::|||
648 AaPmetValSerSerMetGluSerAaPValAlaThrIleGlySerValArgAlaAaP 667
      ::|||::|||::|||
2191 GAAGCGCGCTCAATTTATTTGAGCATATTTTGGCAGTTTCCAGGTGAAAG----- 2241
      ::|||::|||::|||
668 SerGluAlaLeuProArgMetAaPAlaArgThrAlaGluAaIleValSerLySlyrGln 687
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2242 -----CAATATATGTGACAAACATTGTGCAAGAA--GCG 2271
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688 LyelIeLySerLeuAlaPheGlyProAaPHisArgIleGluMetLeuProGluValLeu 707
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2272 AAAAATAAAGGATATGTGACAGACGCTGCTGATCGGCGCGCTATTTTCCGATTTTACA 2331
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708 AaPglyArgMet--LeuLySileTrpThrAaPArgAlaIa--GluThrAlaGluLeu 725
      ::|||::|||::|||
2332 AGCGGCAACTCAACGTCGCCAGCTGCGCCAGCGGAGCGGAGTGAACACACCGATCCA 2391
      ::|||::|||::|||
726 GlyLeuValLyTrAaPtyrThrLeuLeuLySerValAaP--SerValThrValSer 744
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745 AlaAaPglyThrArgAla-----LeuValGluAla 754
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2449 GAAGAACGCGCTGACAGCGCGCTGTGCTGCAAGTGCATGACGAATCAATTTTGAAGCG 2508
      ::|||::|||::|||
755 ThrLeuGluJusSerAlaCyLeuSerAaPLeuValHisProGlu 769
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2509 CCGAAAGAGAAATGACAGCGGCTGTGCGCGCTCGT--CGAGG 2550
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RESULT 9
PCT-US95-04080-33
/ Sequence 33, Application PC/TUS9504080
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
/ TITLE OF INVENTION: STEAROTHERMOPHILUS
/ NUMBER OF SEQUENCES: 34
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/04080
/ FILING DATE:
/ CLASSIFICATION:
/ INFORMATION FOR SEQ ID NO: 33:

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SEQUENCE CHARACTERISTICS:	
LENGTH: 2631 base pairs	
TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: DNA (genomic)	
FEATURE:	
NAME/KEY: CDS	
LOCATION: 1..2631	
PCT-US95-04080-33	
Alignment Scores:	
Pred. No.:	0.000192
Score:	136.50
Percent Similarity:	37.2%
Best Local Similarity:	21.3%
Query Match:	3.4%
DB:	6
US-10-600-070B-2 (1-801) x PCT-US95-04080-33 (1-2631)	
QY	12 SerProphgelnleuCybA-gleuProProalathThrlsyleuarghSerhsaen 31
DB	47 GCGCTTTTTCGCGCTTGCCTTTGGATACGATTAAGGAGATTCAAGAACGAGCTT 106
QY	32 ThserthrthrlleCySerlaserlyeTrrAlaaphargleuenserAephnen 51
DB	107 ACGGTTACGATGATGTTAAACAAATTTTGGCGGAGAGACGCCGACCCACATTTCTG 166
QY	52 PhehrSerapSerSerSerSerPhealathrlaThr-----Thtrhrla 68
DB	167 TCGCGCTTT-GACGCCGGGAAAAACAGCTTCGCCCATGAACGTTCCAAAGCGGAAAGGC 225
QY	69 ThrlleuValserleuProSerlleaphargProgluarghlsvalProlleprole 88
DB	226 GCGCGGCAGACAGCGCCCGGAACTGCGAAGCAGTTTCCGCTGCGCGAATTGCTC 285
QY	89 AephPheTyrGlnValleuglyValagln---ThrlsPheleuThrraPglylleargarg 107
DB	286 AAGCGCTACCGGATCCCGCTATAGAGTCCGACTTTCGAAGCGACGATTTATCGGA 345
QY	108 AlaPheglualAargValserlySerProglInPheglyPheSeraspapAlaleulle 127
DB	346 ACGATGCGCGCGCGGCTGACGAGAA-----GGGTTTCAGTGAAGTCATTTCC 396
QY	128 SerargarglnleuenglualaAalacygluThrlleuSeranProargSerargarg 147
DB	397 GCGACCGCATTTAACCCG-----CTTGCTTCCCGCAAGTCAGCGTG 441
QY	148 GlnTyr---AsnglueglyleuLeuapapPgluglualaThrVallleThraspVal--- 165
DB	442 GAGATTTCGAAAAAAGGAGATTACCGACATCGATCGTACCCCGGAGACGAGTCGTGAA 501
QY	166 -----Protrp 167
DB	502 AAATACGGCTCACCCCGAGCAAAATTGTCGATTGAAGATTGGCGCAGCAAAATCC 561
QY	168 AspIysValProgly-----AlaleuCybValleuglnglu 179
DB	562 GACAAACATCCTGGCGGTGCCCGGATCGGGAAAAAACGCGCTCAAGCTGCTCAAGCA 621
QY	180 GlyglygluThrglulleValleuargValGlyglualaleuLeuuyegluargleuPro 199
DB	622 TTCGCGACAGGTGAAACGTACTGCATTCGATCGATGAGATCAAAAGGCGAAGAGCTGAA 681
QY	200 LysSerPheIysgln-----AspValValleuValIecalaLeuAlaPheleuapVal 217
DB	682 GAAATTTGGCGCAATCCGGAATTGGCGCT---TTAAGCAAAACAGCTGGCCGCTATT 738
QY	218 SerArgaspAla-----MecAlaleuapSerProPrahPheilleThnglyTyrglu 234
DB	739 TGGCGGAGACGCCCGGATTGAGCTGACGCTCAT-----GACATTGCTTCAAAAGGAGA 792


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QY 235 phevalgluinalaleuyleuengluaglialaserleuualaproasp 254
DB 793 GACCGGAAAAGTGGCTGCTGTTTCAGAGCTCGGATTCAGTCGTTTCAGACAG 852
QY 255 leuarglialgluileuarglu-----thrleu 263
DB 853 ATGGCGGTCCAAACGGATGAGGCGAAAGCGCTGCGCGGATTTGGCATCGCC 912
QY 264 glugluilethrproarglyrvalleugluileuylleu-----proleugly 280
DB 913 GACAGCGTACCGGACGAAATGCTCGCGGACAAAGCGCCCTCGTGTGAGGTGGG 972
QY 281 asparpyr-alaalalyargleuanglyleuserglyvalargasnilleuutpse 300
DB 973 GACACTATACCATCCCGGATGTTCGGGATCGCT-----TGGCC 1014
QY 300 ryalglglyglglyalaser-alaaleuvalglylyleuthragluylpshemeca 320
DB 1015 AACGAACGCGGCGGCTTTCTCGCGCGGAGACGCGCGCTCGCATCCGAATTTCTC 1074
QY 320 hngluialphe----- 323
DB 1075 GCTTGCGTGGCGATGACGAAAGAAAACGATTTGATTCAAGCGCGCGCGCTC 1134
QY 324 -----leuargmetthrilaalagluinal-aspleuaphevalalathr 338
DB 1135 GCGCTAAATGGAAGGATTCGACGCGCGCTGTGTGATGTGTGCTGCGCGCT 1194
QY 339 proserasnilleuproalaguser-----phegluvaltyrglu 351
DB 1195 TACTTGCTCGATCCGCGCGGCGCGCGCGGACGTTGCGCGCGGAAATGATCAG 1254
QY 352 valalaleuualaleuvalaglinalpheilleglylvs----- 364
DB 1255 TACGAGCGCGTGCATCGGATGAGCGGTCTATGGAAGGAGCGGACGCGTTCCT 1314
QY 365 ---lysptronileuengluinalapralasrlysgluinphenglingleuagluinallys 383
DB 1315 GATGAACGACCGCTTCCGAGCATCTCGCCCG-----AAGCGCGCGCGC 1359
QY 384 valmetalametgluileuproalameleuetyraserthrargasnantpirlu---ile 402
DB 1360 ATTTGGGCGCTTGAAGAGCGGTGATGACGAACTGCGCGGACGAAACAGATCGCGCTG 1419
QY 403 aspheuglyleugluargglyleucysalaleuileglyl----- 416
DB 1420 CTGACCGAGCTGAACAGCGCGTGGCTGGCCATTTGGCCAAATGGAATTTACTGAGCTG 1479
QY 417 lysvalasrplycyatgmet---trpleuglyleuasp---sergluapserglintyr 434
DB 1480 AAGGTGACACGAAAGCGCTTGAACAGATGGGCGGAGCTCAACGAGCACTGCAG--- 1536
QY 435 argaenproalailevalgluphevalleugluasnserasnargasrapsnaspap 454
DB 1537 -----GGGTGAGCGGCGGCAATTTCGAACCTCGCGGCGGAGAGTTCAACATTAC 1587
QY 455 leuproglyleucyaleuileuengluinthrpleuualaglyvalalpheproargphe 474
DB 1588 TCGCCG-----AACAGCTCGGAGCG-----GTTTATTTGACATGAGCTG 1626
QY 475 argaerthrlyasrplyslypheleuglyasrpyrtyrasrapsrprometvalleu 494
DB 1627 CAGCTCCCGGTGTTGAAAGACAAAGACCGGCT---TATTCGACTTCAGCCGATGTGCT 1683
QY 495 serlyrleu---gluargvalagluvalalagnglyserproleuualalaalathr 513
DB 1684 GAGAGCTTGCACCGGACATGAAATCGTGAA-----CAATATTTGCAATTACGCCAA 1737
QY 514 metalaargileglyalagluhiivallybalaseralametgluialeugluylsval 533
DB 1738 CTCGCGAAGCTGCGAGTCAACGTATATTGAA---GGGCTGTGAAAGTGTGACCCCGCTG 1794
QY 534 pheproserargtyrthrapsrargasnerralagluprolayasrvalagluinthr--- 552

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DB 1795 ACGGCGAAAGTGCACACGATGTTCATACAGCG-----TTGACGCAACCGCG 1842
QY 553 ---valpheaser-Valasrprovalaglyasnasnvalaglyargaspolygluproglyval 571
DB 1843 CGCTCAGCTCCGTGACACCGAATTTGCAAAACATTCGATTCGCTTGAGGAGGCGCG 1902
QY 572 pheilealagluialavalargproserglu-----asnpe 583
DB 1903 AAAATTCGCGAGCGGTTCGCTGCGTGGAGCGGAGCTGCTCATCTTTCGCGCGCAT 1962
QY 584 glutrarnasrpyralialeargalaglyvalsergluseraservalaspgluthrthr 603
DB 1963 TCGCAATAGACTGCGCGCTCTCGCCCATATCGCGAA-----GATGCAATTTG 2013
QY 604 valglu-----metservalalasp 610
DB 2014 ATTTGAAGCGTTCGCGCGGTTGGACATCCATACGAAACAGCCATGACATTTTCAT 2073
QY 611 metleuylsglu-----Alaservallyleleuualaglyvalalalegly 627
DB 2074 GTGACGGAAGAGAGCTGACACGCAACATGCGCGCGGACGAGCGCTCAATTTTGGC 2133
QY 628 leuileserleuphesergluylslyrphleuylsersersersersphegluarglys 647
DB 2134 ATCGTGTACGCGATTAAGTAT---TACGCTGCGGCAAACTTGAACTTAACGCGCAAA 2190
QY 648 aspmetvalsersemecgluseraservalalathrilleglyservalargalaspap 667
DB 2191 GAAGCGGTGAATTTATGAGGATATTTTGGCAGATTTTCCAGGTGAAG----- 2241
QY 668 serglualaleuproargmetasrpalargthrilaaglualasnillevalserlystrpirlu 687
DB 2242 -----CAATATGACAACTTGTGCAAGAA---GCG 2271
QY 688 lysileyserserleualasrheglyproasrphisargilleglumetleuproglyualleu 707
DB 2272 AAAAAGGATGATGTGACGACGCTGCGCATGCGCGCGCTATTTGCGCATTTTAA 2331
QY 708 asrplyargmet---leuylsillethrthrapsrargalala---gluthralagluileu 725
DB 2332 AGCGCAACTTCACAGCGCTTCCGCGGAGCGGACGCGCATGACACCGATCCAA 2391
QY 726 glyleuvaltyrasrpyrthrleuileuylsleuservalasp---servalthralsr 744
DB 2392 GGGAGTCCGCTGAT---ATTATTAAGGATGATGATCTAAGCGTGAAGCTGCGC 2448
QY 745 alaasrplythrargala-----leuvalgluiala 754
DB 2449 GAAGAACGCTGACAGCGCGCTGTGCTGCAAGTGCATGACGAATCATTTTGAAGCGC 2508
QY 755 thrleugluinseralacyleuserasrpleuvalhisproglu 769
DB 2509 CCGAAAGAGAAATCGAGCGGCTGCGCGCTCGTT---CCAGAG 2550

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RESULT 10
 US-08-436-664-21
 ; Sequence 21, Application US/08436664
 ; Patent No. 5874282
 ; GENERAL INFORMATION:
 ; APPLICANT: RIGGS, MICHAEL G.
 ; APPLICANT: STIVAM, MATTHEW
 ; APPLICANT: TUDOR, STANLEY D.
 ; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Gen-Probe Incorporated
 ; STREET: 9880 Campus Point Drive
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92121

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,664
FILING DATE: 08-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/394,232
FILING DATE:
APPLICATION NUMBER: 08/307,410
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: 08/222,612
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: GP94003.CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 2631 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURES:
NAME/KEY: Coding Sequence
LOCATION: 1...2628
OTHER INFORMATION:
US-08-436-664-21

Alignment Scores:
Pred. No.: 0.000323
Score: 134.50
Percent Similarity: 37.1%
Best Local Similarity: 21.5%
Query Match: 3.3%
DB: 2
Gaps: 45

US-10-600-070b-2 (1-801) x US-08-436-664-21 (1-2631)
QY 12 SerProPheGlnLeuCyArgLeuProProAlaThrThrLysLeuArgSerHisAsn 31
DB ::::|||||
QY 47 GCGCCCTTTTCGCGTTCGCGCTTTTGCATACGATTAAGGATTCATACGACGAGCT 106
QY 32 ThrSerThrThrLleCySerSerLaserLysTTPAlaAspArgLeuSerAspPhean 51
DB :|||
QY 107 AGCGGTTTACGATGATGTTAAACAAATTTCGCGAAGACGCGGACCATTCCTG 166
QY 52 PheThrSerAspSerSerSerSerPheAlaThrAlaThr----- 65
DB :|||
QY 167 TGGCGTTT-GACGCGCGGAAACGACGTTCCGCGCATGAACGTTCCAGACTATTAAGC 225
QY 66 -----ThrThralThrLleuValSerLeuProProSerLleAspArgProGlu 81
DB :|||
QY 226 GCGCGCGACAGACGCGCGCGGAACTGTGGAACACTTTCGCTGCGCGCAATTGCTC 285
QY 82 ArgHisValAlaProLleProLleAspPheTyrgLlnValLeuGlyAlaGlnThrHisPheLeu 101
DB ::::|||||
QY 286 AAGGCGTACCGCATCCCGCC-----TTAGAGCTC-----GACCATTTACGA 327
QY 102 ThrAspGlyLleArgArgAlaPheGlnAlaArgValSerLysProProGlnPheGlyPhe 121
DB :|||
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DB 328 GCGGACGATATTATCGAAGCAGTGGCGCGGCTGACGAGAA-----GGCTTT 378
QY 122 SerAspAspAlaLeuLleSerArgArgGlnLleuGlnAlaAlaCySGluThrLeuSer 141
DB ::::|||||
QY 379 GCACTGAAAGTCATTTCCGCGGACCGCGGATTTAACCGA-----CTTGCT 423
QY 142 AsnProArgSerArgArgGlyTyT--AsnGlnGlyLeuLeuAspAspGlnGlnAlaThr 160
DB ::::|||||
QY 424 TCCCGCGAAGTACGACGCTGAGATTAACGAAAAAGGATTAACGACATCGAGTCGACG 483
QY 161 ValLleThrAspVal----- 165
DB :|||
QY 484 CCGGAGACGTCGTGGAATAATACGGCTCACCCCGGACGAAATTTGCACTTGAAAGGA 543
QY 166 -----ProTTPAspLysValProGly-----Ala 173
DB :|||
QY 544 TTGATGGCGGCAAAATCGACACATCCCTGCGTCCCGGCGCATCGGGAATAAACGCC 603
QY 174 LeuCyValLeuGlnGlnGlyGlyGluThrGlnLleValLleuArgValGlyGlnAlaLeu 193
DB ::::|||||
QY 604 GTCAAGCTGCTCAAGCAATTCGCGACCGGTGCAAAACGTACTGCGATCGATGAGATTC 663
QY 194 LeuLysGlnArgLeuProLysSerPheLysGln-----AspValValLeuValMetAla 211
DB :|||
QY 664 AAGCGGAGAAAGCTGAAGAAATTTGCGCAATACCGGATTTGGCGCTT--TTAGC 720
QY 212 LeuAlaPheLeuAspValSerArgAspAla-----MetAlaLeuAspProProAsp 228
DB :|||
QY 721 AAACAGCTGGCGGCTATTTGCGGACGCCCGCGGTGAGCTGACGCTGAT-----GAC 774
QY 229 PheLleThrGlyTyrgLlnPheValGlnGlnAlaLeuLysLeuLeuGlnGlnGlyAla 248
DB ::::|||||
QY 775 ATTGCTCAAAAGAGAAAGACCGGGGAAAGGTGTGCTGTTCGAGACCTCGATTC 834
QY 249 SerSerLeuAlaProAspLeuArgAlaGlnLleAspGlu----- 261
DB :|||
QY 835 CAGTCTTTTCGACAGATGCGCGCTCCAAACGAGATGAGGCGGAAACCGCTCGCGGG 894
QY 262 -----ThrLeuGlnGlnLleThrProArgTyrgValLeuGlnLeuLysLeu 277
DB :|||
QY 895 ATGATTTTGCATGCGCGGACGACGCTCACGAGCAAGAAATTCGCGGACAAAGCGGCGCT 954
QY 278 -----ProLeuGlyAspAspTyT-AlaAlaLysArgLeuGlnGlyLeuSerGlyVa 294
DB ::::|||||
QY 955 GTCGTGAAGTGTGGCGGACAACTATCACTATGCCCCGATTTGCGGATCGCCT----- 1009
QY 294 LArgAsnLleLeuTTPSerValGlyGlyAlaSer-AlaLeuValGlyGlyLeuT 314
DB :|||
QY 1010 -----TGGCCACGAAACGCGGCGGTTTCTGCGCGCGGACGCGCTC 1056
QY 314 hrArgGlnLysPheMetAsnGlnAlaPhe----- 323
DB :|||
QY 1057 GCGGATCCGAAATTTCTCGCTTGGCGATGAGAGAAAGAAACATGTTGTAT 1116
QY 324 -----LeuArgMetThrAlaAlaGlnGlnVal- 332
DB :|||
QY 1117 TCAAGCGGCGCGCGCTGCGCTAAATGAAAGGAAATGAACTGCGCGGCTGCTTC 1176
QY 333 AspLeuPheValAlaThrProSerAsnLleProAlaGlnSer----- 346
DB :|||
QY 1177 GATCTGTGCTGCGCTTACTTCTGATCCGCGGCGGCGGCGGCGGACCTGCGCG 1236
QY 347 ---PheGlnValTyrgLlnValAlaLeuValAlaGlnAlaPheLleGlyLys--- 364
DB :|||
QY 1237 GTGGGAAAAATGATCAATGACAGCGCGGTGCGATGAGGCGGTCTATGAAAGGA 1296
QY 365 -----LysProHlValLeuLeuGlnAspAlaAspLysGlnPheGln 377
DB :|||
QY 1297 GCGAAGCGGACGCTTCGATGAAACGACGCTTGGCGGACATCTGCGCGC----- 1347
QY 378 GlnLeuGlnGlnAlaLysValMetAlaMetGlnLleProAlaMetLeuTyrgThrArg 397
DB :|||
QY 1348 -----AAGCGCGGCGCATTTGGCGCTTGAAAGCGGTTGATGACGAACTGCGCGCG 1401
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US-08-436-664-31

Alignment Scores:
 Pred. No.: 0.000323 Length: 2631
 Score: 134.50 Matches: 194
 Percent Similarity: 37.1% Conservative: 141
 Best Local Similarity: 21.5% Mismatches: 357
 Query Match: 3.3% Indels: 212
 DB: 2 Gaps: 45

US-10-600-070B-2 (1-801) x US-08-436-664-31 (1-2631)

QY 12 SerProheGlnLeuCyArgLeuProProAlaThrThryLeuArgSerHisben 31
 DB 47 GCGCTTTTTCGCGTTCGCGCTTTTGCATACGATTAAGGAGTTCATACGACGAGTCT 106
 QY 32 ThrserrThrThryCySerAlaSerlySTPAlaSprArgLeuSerAspPhean 51
 DB 107 ACGGCTTACAGATGATTAACAAATTTTGGCGAGAGACGCCGACCCACATCTCTCG 166
 QY 52 PheThrSerAspSerSerSerSerSerPheAlaThrAlaThr----- 65
 DB 167 TGGCGTTT-GACGCGCGGAAACGACGTTCCGCGCATGAACCTTCCAGACTTTAAAGCC 225
 QY 66 -----ThrThralThrLeuValSerLeuProProSerThleAspArgProGlu 81
 DB 226 GGGCGCGCAGACACCGCGCGGAACTGTGCGAAACAGTTCCGCTGCGCGAATTGCTC 285
 QY 82 ArgHisValProIleProIleAspPheThryGlnValLeuGlyAlaGlnThrsPheLeu 101
 DB 286 AAGGCGTACGCGATCCCGCC-----TATGAGCTC-----GACCATTCAGAA 327
 QY 102 ThrAspGlyThleArgArgAlaPheGlnAlaArgValSerLySerProProIlnheGlyPhe 121
 DB 328 GCGGACGATATATTCGAAACGATGCGCGCGCGCGTACGACGAGAA-----GGGTTT 378
 QY 122 SerAspAspAlaLeuIleSerArgArgGlnIleLeuGlnAlaAlaCySerGlnThrLeuSer 141
 DB 379 GCGTGAAGATCATTTCCGCGCAGCCGCGATTAACCCAG-----CTTGCT 423
 QY 142 AsnProArgSerArgArgGlnThyr--AasnGlnGlyLeuLeuAspAspGlnGlnAlaThr 160
 DB 424 TCCCGCAGATGACGCGTGAATTCAGAAACGATTAACGACATCGATCGTACAG 483
 QY 161 ValIleThrAspVal----- 165
 DB 484 CCGGACGCGTGTGAAACAAATACGCGCTCACCCCGGACGAAATGTGCACTTGAAGAA 543
 QY 166 -----ProThrAspLySerValProGly-----Ala 173
 DB 544 TTGATGCGCGCAAAATCCGACAAATCCTCGGCGTGCAGCGCATCGCGGAAAAAAGACGC 603
 QY 174 LeuCyValLeuGlnGlnGlyGlnThrglnIleValIleuArgValGlyGlnAlaLeu 193
 DB 604 GTCAGACTGCTCAAGCAATTCGCGCAGCGTGAAGAACTACTGCGATCATCATGATGATC 663
 QY 194 LeuLySerGlnArgLeuProLySerPheLySerGln-----AspValValLeuValMetAla 211
 DB 664 AAGGCGAAGAGCTGAAGAAATTTGCGCGCAATACCGGATTTGCGCTT-----TTAAGC 720
 QY 212 LeuAlaPheLeuAspValSerArgAspAla-----MetAlaLeuAspProAsp 228
 DB 721 AAACAGCTGCGCTATTGCGCGACGCGCGCGTGGAGTGAAGCTCAT-----GAC 774
 QY 229 PheIleThrglyThryGlnPheValGlnGlnAlaLeuLySerLeuGlnGlnGlnGlyAla 248
 DB 775 ATTGTCTACAAAGAGAGACCGGGAAGAGTGCTGCGCTTGTTCAGAGAGCTCGGATTC 834
 QY 249 SerSerLeuAlaProAspLeuArgAlaGlnIleAspGln----- 261
 DB 835 CAGTCTTTCTCGACAAAGATGCGCGCTCAACCGATGAAGCGAAAAAGCGCTCGCGCG 894
 QY 262 -----ThryLeuGlnGlnIleThrProArgThryValLeuGlnLeuLeuGlnLeu 277

DB 895 ATGATTTTGGATGCGCGCATCGCTCAAGACGAAATATGCTGCGCGCAAAAGCGGCTTC 954
 QY 278 -----ProLeuGlyAspAspThyr-AlaAlaLySerLeuAsnGlyLeuSerGlyVal 294
 DB 955 GTCTGAGAGTGTGTGGGACAACTATACCAATGCGCGCATTTGTGCGGATGCGCTC----- 1009
 QY 294 LArgAsnIleLeuThrPserValGlyGlyAlaSer-AlaLeuValGlyGlyLeuT 314
 DB 1010 -----TGGCAACGAAAGCGCGGCTTTTCTGTGCGCGCGAGACGCGGCTC 1056
 QY 314 hArgGlnLyPheMetAsnGlnAlaPhe----- 323
 DB 1057 GCCGATCCGAAATTTCTGCTTGTGCGATGAGACGAAAGAAAAACGATTTTGAT 1116
 QY 324 -----LeuArgMetThralAlaGlnGlnVal- 332
 DB 1117 TCMAAGCGGCGCGCGCTGCGCTAAATGAAAGAAATCGAACTGCGCGCTGCTTC 1176
 QY 333 AspLeuPheValAlaThrPserAsnIleProAlaGlnSer----- 346
 DB 1177 GATCTGTGCTGCGCGCTTACTTGTCTGATCGCGCGCAGCGCGCGACGTTGCCGCG 1236
 QY 347 ---PheGlnValThryGlnValAlaLeuAlaLeuValAlaGlnAlaPheIleGlyThyr--- 364
 DB 1237 GTGGCAAAATGCAATCAATGACGAGCGGTGCGATGAGAGCGGCTCTTATGAAGAA 1296
 QY 365 -----LyProHISLeuLeuGlnAspAlaAspLySerGlnPheGln 377
 DB 1297 GCGAAGCGGACGCTTCTGATGAACCGACGCTTCCGAGCATTCGCGCCG----- 1347
 QY 378 GlnLeuGlnGlnAlaLyValMetAlaMetGlnIleProAlaMetLeuThyrAspThryArg 397
 DB 1348 -----AAGCGCGCGCGCATTTGGCGCTTGAAGAGCGGTGATGAGCAACTGCGCGCG 1401
 QY 398 AsnAsnThrGln---IleAspPheGlyLeuGlnAlaGlyLeuCyAlaLeuLeuIleGly 416
 DB 1402 AAGCAAAAGATCGCTGCTGACCGACGCTCGAACGCGCTGCGCATTTTGGCCAT 1461
 QY 417 -----LyValAspGlyLucyAspMet---TrpLeuGlyLeuAsp--- 428
 DB 1462 ATGCAATTTACTGAGTGAAGTGAACGACGAGCGGCTTGAACAGATGGCGCGAGATC 1521
 QY 429 SerGlnAspSerGlnThryArgAsnProAlaIleValGlnPheValLeuGlnAsnSerAsn 448
 DB 1522 ACCGACGAGCTCAG-----GCGGTGAGCGCGCGCATTTACGAACTCCCGCGC 1569
 QY 449 ArgAspAspAsnAspAspLeuProGlyLeuCySlySlyLeuLeuGlnThrThryLeuAlaGly 468
 DB 1570 CAGAGTTCACATTAATCCTCGCG-----AACAGCTCGGAGCG----- 1608
 QY 469 ValIlePheProArgPheArgAspThryAspLySlyPheLySlyLeuGlnIlyAspThry 488
 DB 1609 GTTTATTTGACAGCTGACGCTCCCGCTGTTGAAGAAACAAACAAACGCG-----TATTGG 1665
 QY 489 AspAspProMetValLeuSerThryLeu---GlnArgValGlnValValGlnIlySerPro 507
 DB 1666 ACTTCAGCGGATGTGTTAGAAGCTTGACCGCAGCAACGAAATGCTGCA-----CAT 1719
 QY 508 LeuAlaAlaAlaAlaThrMetAlaArgIleGlyAlaGlnIleValIlyValAlaSerAlaMet 527
 DB 1720 ATTTCGATTAACCGGCAACTCGCAAGCTGACGTCGAACTGAATTAATGA---GGGCTGCTG 1776
 QY 528 GlnAlaLeuGlnIlyValPheProSerArgThryThrAspArgAsnSerAlaGlnProLyS 547
 DB 1777 AAGTGTGACCCCGCTGACGCGGCAAGTGCACAGATTTCAATCAGCG----- 1827
 QY 548 AspValGlnGlnThyr-----ValPheSerValAspProValGlyAsnAsnValGlyArg 565
 DB 1828 ---TTGACGCAACCGGCGCGCTCAGCTCGTGAACGAAATTTGCAAAACATTCGATTC 1884
 QY 566 AspGlyGlnProGlyValPheIleAlaGlnAlaValArgProSerGln----- 581

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Db      1885 CGGCTTGAGAGAGGCGGAAATCCCGACGCGTTCGCGGACCGGACGCTC 1944
Qy      582 -----AsnPhgIuThraaApTYrAlaIleuAglaIyValserGluSer 597
Db      1945 ATCTTGGCGCGGACATTCGCAATATGAGCTGCGGCTCTCGCAATATCGGGAA--- 2001
Qy      598 SerValaspGluThrValGlu----- 605
Db      2002 -----GATGACAAATTGATTGAAGGTTCCGGCGGGGTGGACATTCAGAAAGA 2055
Qy      606 ---MetSerValAlaAspMetLeuIysGlu-----AlaSerValIysIleuAla 621
Db      2056 GCCATGCAATTTTCCATGTGAGCGGAGAAAGCTGACGCCAACATGCGCCCAAGCG 2115
Qy      622 AlaGlyValAlaIleGlyLeuIleserLeuPheSerGlnIlyThrPheLeuIysSer 641
Db      2116 AAGCCGCTCAATTTTGGCATTCGTTACGCGCATTAAGAT---TACGCTGCGCGCAAAAC 2172
Qy      642 SerSerPheGlnArgIysAspMetValSerSerMetGluSerAspValAlaThrIleGly 661
Db      2173 TTGAACATTACCGCGAAGAGAGCGGCTGAATTTATTAAGCGAATTTTCCAGTTTCCA 2232
Qy      662 SerValArgAlaAspAspSerGluAlaLeuProArgMetAlaArgThrAlaGluAsn 681
Db      2233 GGTGTAAAG-----CAATATATGACACAC 2256
Qy      682 IleValSerIyTrpGlnIlyIleYserLeuAlaPheGlyProAspHisArgIleGlu 701
Db      2257 ATTGTGCAAGAA---GCGAAACAAAAGGATATGTGACACGCTGTGATCGGCGCGC 2313
Qy      702 MetLeuProGluValLeuAspGlyArgMet---LeuIylIeTrpThrAspArgAlaIa 720
Db      2314 TATTTCCCGCATTTATCAAGCCGCACTTCAACGTCCGACGCTCCGACGCGAGCGG 2373
Qy      721 ---GluThrAlaGlnLeuGlyLeuValIyAspTYrThrLeuLeuIysSerValaAsp 739
Db      2374 ATGAACACACCGATCCCAAGGAGTGCCTGAT---ATTATTAATAAAGCATGATCGAT 2430
Qy      740 ---SerValThrValSerAlaAspGlyThrArgAla----- 750
Db      2431 CTAAAGCTAGGCTCGCGAAGAACCGCTGACAGCGCGCTGTGTCGACAGTCATGAC 2490
Qy      751 -----LeuValGluAlaThrLeuGluGluSerAlaCysLeuSerAspLeuValHisPro 768
Db      2491 GAACATCATTTTGAAGCGCGCGAAGAGAAATGACAGCGCTGTGCGCCCTCCT 2547
Qy      769 Gln 769
Db      2548 GAG 2550

RESULT 12
US-09-135-642-21
; Sequence 21, Application US/09135642
; Patent No. 6066483
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATHEOK
; APPLICANT: TODOR, STANIA D.
; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/394,232
; FILING DATE:
; APPLICATION NUMBER: 08/307,410
; FILING DATE: 16-SEP-1994
; APPLICATION NUMBER: 08/222,612
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94003.CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..2628
; OTHER INFORMATION:
; US-09-135-642-21

Alignment Scores:
Pred. No.: 0.000323
Score: 134.50
Percent Similarity: 37.1%
Best Local Similarity: 21.5%
Query Match: 3.3%
DB: 3 Gaps: 45

US-10-600-070b-2 (1-801) x US-09-135-642-21 (1-2631)
Qy      12 SerPropheGlnLeuCyAspArgLeuProAlaThrIlyLeuArgTrpSerHisAsn 31
Db      47 GCGCCTTTTTCGCGTTCGCTTTGCAATACGATTAAGGATTCATACGAACGAGCTC 106
Qy      32 ThrSerThrTrileCysSerAlaSerIyTrpAlaAspArgLeuLeuSerAspPheAsn 51
Db      107 ACGGGTTTACGATGATGTTAAACAAATTTTGGCGAAGAGACGCCAGCCACATTTCTG 166
Qy      52 PheThrSerAspSerSerSerSerPheAlaThrAlaThr----- 65
Db      167 TGGCCTTT-GACGCCGGAACAGCGTTCCGCCATGAACCTTCCAGACTATAAGGC 225
Qy      66 -----ThrThrAlaThrLeuValSerIleuProProSerIleAspArgProGlu 81
Db      226 GGGCGGACAGACAGCCCGCGGACCTGCGAACAGTTTCGCTGCGCAATGCTC 285
Qy      82 ArgHisValProIleProIleAspPheTYrGlnValLeuGlyAlaGlnThrHisPheLeu 101
Db      286 AAGGCTACCGCATCCCGCC-----TATAGCTC-----GACCATTAAGAA 327
Qy      102 ThrAspGlyIleArgArgAlaPheGluAlaArgValaSerIyProProGlnPheGlyPhe 121
Db      328 GCGGACGATTTATTCGAAACGATGCGCGCGGCTGACCGAGAA-----GGGTTT 378
Qy      122 SerAspAspAlaLeuIleSerArgTrpGlnIleLeuGlnAlaIaCysGluThrLeuSer 141
Db      379 GCAATGAAGATCATTTCCGCGGACCGCGCATTTAAACCCAG-----CTTGCT 423

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[illegible]

Qy	417	-----LysValaIAspGluCysArgMet-----TrrPleuGlyLeuAsp----	428
Db	1452	ATGGAAATTACTGGAGTGAAGAGTGAACGAAAGCGGCTGTGAACAGATGGGGCGAGCTC	1521
Qy	429	SerGluAspSerGlnTyrArgAsnProIleValGluPheValLeuGluAsnSerAsn	448
Db	1522	ACCGAGCAGCTGCAG-----CGGCTCAGCGCGGCATTACGAATCGCGCG	1569
Qy	449	ArgAspAsnAspAspLeuProGlyLeuCysAlaLeuLeuGluTrrPleuAlaGly	468
Db	1570	CAAGAGTTCAACATTAACTCCGCG-----AAACAGCTCGGAGCG-----	1608
Qy	469	ValValPheProArgPheArgAspThrIleAspIleValSerPheLeuGlyAspTyr	488
Db	1609	GTTTATTATTGACAAAGCTCAGCTCCCGGTGTGAAAAGACAAAACCGCG--TATTGC	1665
Qy	489	AspAspPrometValLeuSerTyrLeu--GluArgValGluValAlaGlySerPro	507
Db	1666	ACTTCAGCCGATGTCCTTGAGAGCTTCACCGCACCACTGAATTCGTGAA-----CAT	1719
Qy	508	LeuIleAlaIleAlaIleThrMetAlaArgIleGlyAlaGluIleValIleAlaSerAlaMet	527
Db	1720	ATTTTGCATTACCGGCACATCGGACAGGTGACATCACTATATTGAA--CGCGTGTG	1776
Qy	528	GlnAlaLeuGlnIleValPheProSerArgTyrThrAspArgAsnSerAlaGluProIle	547
Db	1777	AAAGGTGTGCACCCCGTTACGCGGCMAATGCAACGATTTCAATCAGCG-----	1827
Qy	548	AspValAlaGlnIuThr-----ValPheSerValAspProValGlyAsnAsnValGlyArg	565
Db	1828	--TTGACGCAAAACCGGGCGCTCAGCTTCGTTCMAACGAATTGCAAAACATTTCCGATT	1884
Qy	566	AspGlyGluProGlyValPheIleAlaGluIleValaIleArgProSerGlu-----	581
Db	1885	CGGCTTGAGAAAGGCGGAAATCCGACAGGGTTCTGCGCTGCGAGCCGCACTGCGTCT	1944
Qy	582	-----AsnPheGluThrAsnAspTyrAlaIleArgAlaGlyValSerGluSer	597
Db	1945	ATCTTTGCGCGCGCATCTATTCCGAATTCAGCTGCGCGCTCCGCCCATATCGGGA--	2001
Qy	598	SerValaAspGluThrThrValGlu-----	605
Db	2002	-----GATGACAAATTGATTGAAACGCTTCGCGCGGGTTGACATCATCGAAACA	2055
Qy	606	---MetSerValAlaAspMetLeuIleGlu-----AlaSerValIleLeuIle	621
Db	2056	GCATGTGACATTTCATCTGTAGCGAAGAAAGCTGACGCAACATCGCGCGCAACG	2115
Qy	622	AlaGlyValAlaIleGlyLeuIleSerLeuPheSerGlnIleTyrPheLeuIleSerSer	641
Db	2116	AAGGCGGTCAATTGTGGCATCTGTACGCGCATTAAGTATGAT--TACGGTCTGGCGCAAAAC	2172
Qy	642	SerSerPheGlnArgIleAspMetValSerSerMetGluSerAspValAlaThrIleGly	661
Db	2173	TTGAACATTACCGCGCAAAAGACCGGCTGAATTTATTGAGCATATTTTGCCAGTTTCCA	2233
Qy	662	SerValArgAlaAspAspSerGluAlaLeuProArgMetAspAlaArgThrAlaGluAsn	681
Db	2233	GGTGTAAC-----CAATATATGACAAC	2255
Qy	682	IleValSerIleTrrPleuIleIleIleYsSerIleuAlaPheGlyPProAspIleArgIleGlu	701
Db	2257	ATTGTGACAGAA--GCGAAACAAAAGGGTATGTGACAGCGCTGCTGATCGCGCGCGC	2311
Qy	702	MetLeuProGluValLeuAspGlyArgMet---LeuIleIleTrrPThrAspArgIleAla	720
Db	2314	TATTGTCCCGCAATATACAGCCGCAACTTCAACGTCCGACGCTTGCGCGACGAGCGCG	2377
Qy	721	---GluThrAlaGlnLeuGlyLeuValTyrAspTyrThrLeuLeuIleLeuSerValAsp	739
Db	2374	ATGACACACCCGATCCAGAGGAGTGGCTGAT--ATTATTAAAAAAGCATGATCAT	2433
Qy	740	---SerValThrValSerAlaAspGlyThrArgAla-----	750

Db	2431	CPAACCGTGAAGGCTGCGCGAAGAACGCGCTGCAGGCGCGCTGTTCTCTCAAGTCGATAC	24308
QY	751	-----LaeValgIuAlaThrlengIuGluSerAlaCySleuSerAspLaeValhiAfro	768
Db	2491	GAATCATATTGGAGGCGCGAAGAAAGGAATCGAGCGCGCTGTGCGCGCTGTT---CCA	2547
QY	769	GIU 769	
Db	2548	GAG 2550	
RESULT 13			
US-09-135-642-31			
; Sequence 31, Application US/09135642			
; Patent No. 6066483			
; GENERAL INFORMATION:			
; APPLICANT: RIGGS, MICHAEL G.			
; APPLICANT: SIVARAM, MATTHOOR			
; APPLICANT: TUDOR, STARRA D.			
; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS			
; TITLE OF INVENTION: STEAROTHERMOPHILUS			
; NUMBER OF SEQUENCES: 34			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Gen-Probe Incorporated			
; STREET: 9880 Campus Point Drive			
; CITY: San Diego			
; STATE: CA			
; COUNTRY: USA			
; ZIP: 92121			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSeq Version 1.5			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/135,642			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/394,232			
; FILING DATE:			
; APPLICATION NUMBER: 08/307,410			
; FILING DATE: 16-SEP-1994			
; APPLICATION NUMBER: 08/222,612			
; FILING DATE: 16-SEP-1994			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Fisher, Carlos A			
; REGISTRATION NUMBER: 36,510			
; REFERENCE/DOCKET NUMBER: GP94003.CP2			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 619-535-2807			
; TELEFAX: 619-546-7929			
; TELEX:			
; INFORMATION FOR SEQ ID NO: 31:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 2631 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
; FRAGMENT TYPE:			
; ORIGINAL SOURCE:			
; FEATURE:			
; NAME/KEY: Coding Sequence			
; LOCATION: 1...2631			
; OTHER INFORMATION:			
US-09-135-642-31			
Alignment Scores:			
Pred. No.: 0.000323 Length: 2631			
Score: 134.50 Matches: 194			

[illegible]

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Db      955 GTCTGAGAGTGTGGGCGAACAATGACCATGCCCGGATGTCGGAGTCGCT----- 1009
Qy      294 lArghenlleuTpservAlglylglYAlaser-ALaleuValglYglYleuT 314
Db      1010 -----TGGCCAAAGACGCGCGGCTTTTCTGCGCCGAGAGCGCGCTC 1056
Qy      314 hArsglulYpPheMeAenGluAlaPhe----- 323
Db      1057 GCCGATCCGAAATTTCTGCTTGCTTGCGCATGAGACGAGAAAAAAGATGTTGAT 1116
Qy      324 -----LeuArgMetThrAlaAlaGluGluVal- 332
Db      1117 TCAAAGCGGCGCGCGCTGCGCTAAATAGAAAGAAATGAACTGACGCGCGCTGCTGTC 1176
Qy      333 AepLeuPheValAlaThrProserenlleProAlaGluSer----- 346
Db      1177 GATCTGTGTCGCGCGCTTACTTGTCTGATCCGCGCGAGCGCGCGCGCGCGCTGCGCG 1236
Qy      347 ---PheGluValTyrGluValAlaLeuAlaLeuValAlaGluAlaPheTlleglYlYs--- 364
Db      1237 GTGGCGAAATGATCATGACAGAGCGCGCGATGCGATGAGCGCGCTCATGGAAGAAAGGA 1296
Qy      365 -----LysProHleuLeuGluAlaAspAlaAspLysGlnPheGln 377
Db      1297 GCGAAGCGGACGCTTCTGATGACGAGCGCTTGCGGACATCTGCGCGC----- 1347
Qy      378 GlnLeuGlnGlnAlaYsValMetAlaMetGluTlleProAlaMetLeuTyrAspThrArg 397
Db      1348 -----AAGCGCGCGCGCTTGTGGCGCTTGAAGAGCGCTGTATGAGCAATCGCGCGC 1401
Qy      398 AenAenTpsglu---lleAepheglYleuGluArglYleuCyAlaLeuLeuTlleglY 416
Db      1402 AACGAAACAAGATCGCTGCTGACCGAGCTGCAACAGCGCGCTGCGCATTTTGGCGCAT 1461
Qy      417 -----LysValAspGluCyAspMet---TrrleuGlyLeuAsp--- 428
Db      1462 ATGGAATTTACTGAGTGAAGTGAAGTGAACGAGCGCGCTTGAACAGATGCGCGCGAGCTC 1521
Qy      429 SerGluAspSerGlnTyrArgAsnProAlaTlleValGluPheValLeuGluAsnSerAsn 448
Db      1522 ACCGAGCAGCTGACG-----GCGGTGAGCGCGCGCTTTTACCAATCGCGCGC 1569
Qy      449 ArgAspAspAsnAspAspLeuProGluYleuCyLysLeuLeuGluTrrleuAlaGly 468
Db      1570 CAAGAGTTCAATTAATCTCGCG-----AAACACTCGCGAGC----- 1608
Qy      469 ValValPheProArgPheArgAspThrLysAspLysLysPheLysLeuGluYAspTyrTyr 488
Db      1609 GTTTATTGACAAAGCTGACGCTCCCGGTGTAAGAAACAAACAAACCCGCG---TATTGCG 1665
Qy      489 AspAspProMetValLeuSerTyrLeu---GluArgValGluValAlaGlnGlySerPro 507
Db      1666 ACTTCAGCGATGTGCTTGAAGAGCTTGACCGGACACCAATGAATGCTCGAA-----CAT 1719
Qy      508 LeuAlaAlaAlaAlaThrMetAlaArgLleGlyAlaGluTlleValLysAlaSerAlaMet 527
Db      1720 ATTTCGATTACCGCAACTCGGCAAGCTGCACTCAACGTAAATTTGAA-----GGCGTCGCG 1776
Qy      528 GlnAlaLeuGlnLysValPheProSerArgTyrThrAspArgAsnSerAlaGluProLys 547
Db      1777 AAAGTGTGACACCCCGTGAAGCGGCAAGTGCACATGTTCAATCAGCGC----- 1827
Qy      548 AspValGlnGluThr-----ValPheSerValAspProValGlyAsnAsnValGlyArg 565
Db      1828 ---TTGACGCAAAACCGGCGCTCAGCTCCGTCGAAACCAATTTGCAAAACATTCCGATT 1884
Qy      566 AspGlyGluProGlyValPheTlleAlaGluAlaValArgProSerGlu----- 581
Db      1885 CGGCTTTGAAGAGGCGGAAATCCCGCAGCGCTTGTGTCGCGGAGCGCGCATGCGCTC 1944
Qy      582 -----AsnPheGluThrAsnAspTyrAlaTlleArgAlaGlyValSerGluSer 597
Db      1945 ATCTTTGGCGCGCATATTGCAAAATCGAGCTGCGGTCTCGCCCATATCGCGGAA--- 2001

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Qy      598 SerValAspGluThrThrValGlu----- 605
Db      2002 -----GATGACAAATTTGATGAAGCGTTCCGGCGGCTTGACATCATCAAGAAACA 2055
Qy      606 ---MetSerValAlaAspMetLeuYsGlu-----AlaSerValYsTlleuAla 621
Db      2056 GCCATGGAATTTTCCATGTGAGCGAAGACAGTGAACGACATGCGCAATGCGCGCGCAACG 2115
Qy      622 AlaGlyValAlaTlleGlyLeuTlleSerLeuPheSerGlnLysTyrPheLeuLysSerSer 641
Db      2116 AAGCGCGTCAATTTTGGCATGTGTACGCGCATTAAGTAT---TACGCTTCGCGCAAAAC 2172
Qy      642 SerSerPheGlnArgLysAspMetValSerSerMetGluSerAspValAlaThrTlleGly 661
Db      2173 TTGAACATTAGCGCGAAAGAGCGCGCTGAATTTATTTGAGCATATTTTGGCAGTTTCCA 2232
Qy      662 SerValArgAlaAspAspSerGluAlaLeuProArgMetAspAlaArgThrAlaGluAsn 681
Db      2233 GGTGTAAAG-----CAATATATGAGCAAC 2256
Qy      682 lleValSerLysTrrPglulYsTlleYsSerLeuAlaPheGlyProAspHleArgTlleGlu 701
Db      2257 ATGTGCAAGAA---GCGAAACAAAGAGGTATGTGACAGCGCTGCTCATTCGCGCGCG 2313
Qy      702 MetLeuProGluValLeuAspGlyArgMet---LeuLysTlleTrrThrAspArgAlaAla 720
Db      2314 TATTGGCCGATATATACAAAGCGCAACTTCAACGTCGCACTTGCAGCGCGAGCGCG 2373
Qy      721 ---GluThrAlaGlnLeuGlyLeuValTyrAspTyrThrLeuLeuLysLeuSerValAsp 739
Db      2374 ATGAACACACCGATCCAAAGAGAGTCCGCTGAT---ATTATTAAGAAAGCATGATCAT 2430
Qy      740 ---SerValThrValSerAlaAspGlyThrArgAla----- 750
Db      2431 CTAAAGCGTAGGCTGCGGAAAGACGCTGACAGCGCGCTTCTGCAATGATGAC 2490
Qy      751 -----LeuValGluAlaThrLeuGluGluSerAlaCyLysLeuSerAspLeuValHisPro 768
Db      2491 GAACCTATTTTGAGAGCGCGGAAAGAGAAATCGAGCGCGCTGTGCGCGCTGCT---CCA 2547
Qy      769 Glu 769
Db      2548 GAG 2550

RESULT 14
US-08-394-232A-21
/ Sequence 21, Application US/08394232A
/ Patent No. 6100078
/ GENERAL INFORMATION:
/ APPLICANT: RIGGS, MICHAEL G.
/ APPLICANT: SIVARAM, MATTHEW
/ APPLICANT: TUDOR, STARRA D.
/ TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILUS
/ NUMBER OF SEQUENCES: 34
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Gen-Probe Incorporated
/ STREET: 9880 Campus Point Drive
/ CITY: San Diego
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: IBM Compatible
/ SOFTWARE: FASTSEQ Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/394,232A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/307,410

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Qy 449 ArgAspAspAspAspLeuProGlyLeuCysLeuLeuGluThrTrpLeuAlaGly 468
Db 1570 CAAGGCTTCAATTAACTCCGCG-----AAACAGCTCCGGAAC----- 1608
Qy 469 ValValPheProArgPheArgAspThrLyAspLySlyPheLyLeuGlyAspTyr 488
Db 1609 GTTTATTATTGACAGCTCAGCTCCCGGTGTGAAAAAGACAAAAACCGGC---TATTG 1665
Qy 489 AspAspProMetValLeuSerTyrLeu---GluArgValGluValGluGlySerPro 507
Db 1666 ACTTCAGCCGATGTGCTTGAAGAGCTTCACCGCACCATGAAATGGTGA---CAT 1719
Qy 508 LeuAlaAlaAlaAlaThrMetAlaArgIleGlyAlaGluIleValAlaSerAlaMet 527
Db 1720 ATTTCGATTACCCGCAACTCGGCACAGCTGCAGTCAAGTATATTGAA---CGGTCGCTG 1776
Qy 528 GlnAlaLeuGlnLysValPheProSerArgTyrThrAspArgAsnSerAlaGluProLys 547
Db 1777 AAAGTGTGCAACCCGCTGACCGGCAAGTGCACAGATGTTCAATCAGGCG----- 1827
Qy 548 AspValGlnGluThr-----ValPheSerValAspProValGlyAsnAsnValGlyArg 565
Db 1828 ---TTGACGCAAAACCGGCGCTCAGCTCCGTCGAACCGAATTGCAAAACATTCCGATT 1884
Qy 566 AspGlyGluProGlyValPheIleAlaGluAlaValArgProSerGlu----- 581
Db 1885 CGGCTTGAGAAAGCGCGGAAATCCGCCAGGCTTCGTCGCTCGGAGCCGCACTGGCTC 1944
Qy 582 -----AsnPheGluThrAsnAspTyrAlaIleArgAlaGlyValSerGluSer 597
Db 1945 ATCTTGGCGGCGCATATCGCAATCGAGCTCGCTCCTCGCCCATATCCGGA--- 2001
Qy 598 SerValAspGluThrThyValGlu----- 605
Db 2002 ---GATGACAAATTGATTGAACGCTTCGCGCGGCTTGACATCCATACGAAACA 2055
Qy 606 ---MetSerValAlaAspMetLeuLysGlu-----AlaSerValLysIleLeuAla 621
Db 2056 GCCATGACATTTTCATGTCGACGAAGACGTCGACGCAACATGCGCCGCAAGG 2115
Qy 622 AlaGlyValAlaIleGlyLeuIleSerLeuPheSerGlnLysTyrPheLeuLysSerSer 641
Db 2116 AAGCGCTCAATTTGGCATCGTCGATCGCATTAATGAT---TACGCTGCGCGCAAAAC 2172
Qy 642 SerSerPheGlnArgLysPheAspMetValSerSerMetGluSerAspValAlaThrIleGly 661
Db 2173 TTGAACATTACCGCGAAAGAACCGGCTGAATTATTGACGATATTGTTCCAGTTTCCA 2232
Qy 662 SerValArgAlaAspAspSerGlnAlaLeuProArgMetAspAlaArgThrAlaGluAsn 681
Db 2233 GGTGTAAAG-----CAATATATGACAAAC 2256
Qy 682 IleValSerLysTyrPdnLysIleLysSerLeuAlaPheGlyProAspHisArgIleGlu 701
Db 2257 ATTGTGCAGAA---GCGAAACAAAAGGATATGTCACACGCTGCTGCGCGCGC 2313
Qy 702 MetLeuProGluValLeuAspGlyArgMet---LeuLysIleTyrThrAspArgAlaAla 720
Db 2314 TATTTCGCGATATTAACAAGCCGCACTTCACAGCTGCTGCGCGCGAGCGGCG 2373
Qy 721 ---GluThrAlaGlnLeuGlyLeuValTyrAspTyrThrLeuLysLysSerValAsp 739
Db 2374 ATGAACACACCGATCCAGAGGAGTCCGCTGAT---ATTATTAATAAAGCATGATCAT 2430
Qy 740 ---SerValThrValSerAlaAspGlyThrArgAla----- 750
Db 2431 CTAAAGGTAGGCTGCGCAAGAACGCGTCGACGCGCTGTGCTGCAAGTCATGAC 2490
Qy 751 -----LeuValGluAlaThrLeuGluGluSerAlaCysLeuSerAspLeuValHisPro 768
Db 2491 GAACATCATTTTGGAGCGCGCAAAAGGAATCGACGCGCTGCGCTGCT---CCA 2547
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Db 2548 GAG 2550
RESULT 15
US-08-394-232A-31
; Sequence 31, Application US/08394232A
; Patent No. 6100078
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATHEOOR
; APPLICANT: TUDOR, STALLA D.
; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILU
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,232A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/307,410
; FILING DATE: 16-SEP-1994
; APPLICATION NUMBER: 08/222,612
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fishner, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94003.CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURES:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2631
; OTHER INFORMATION:
; US-08-394-232A-31
Alignment Scores:
Pred. No.: 0.000323 Length: 2631
Score: 134.50 Matches: 194
Percent Similarity: 37.1% Conservative: 141
Best Local Similarity: 21.5% Mismatches: 357
Query Match: 3.3% Indels: 212
Gaps: 45
DB:
US-10-600-070B-2 (1-801) x US-08-394-232A-31 (1-2631)
Qy 12 SerProPheGlnLeuCysArgLeuProProAlaThrThrLysLeuArgArgSerHisAsn 31
Db 47 GCGCCTTTTTCGCGCTTGGCATACGATTAAGGATTCATACGACGACGCTCT 106

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DB 107 ACGGGTTTACATGATGTTAAACAAATTGCGGAGAGACGCCACCATTTCTG 166
QY 52 PheThrSerAspSerSerSerSerPheAlaThr----- 65
DB 167 TGGCGTTT-GACGCCGGAACAGCGTTTCCGCCATGAACCTTAAAGCC 225
QY 66 -----ThThralaThleuValSerleuProProSerleuAspArgProGlu 81
DB 226 GGGCGGACAGACAGCCCGGACCTGCGAACACTTTCGCTGCGCAATTGCTC 285
QY 82 ArgHlAvalProileProileAspPheTyrglnValleuGlyAlaGlnThrHlspheleu 101
DB 286 AAGCGTACCGCATCCCGCC-----TATGAGCTC-----GACCATTAACGA 327
QY 102 ThrAspGlylleArgArgAlaPheGluAlaArgValSerlyProProGlnPheGlyPhe 121
DB 328 GCGGACGATATATATCGAACGATGCGCGCGCTGACGAGAA-----GGGTTT 378
QY 122 SerAspAspAlaLeuileSerArgArgGlnileuGlnAlaAlaCySerGlnThrleuSer 141
DB 379 GCAAGTAAAGTATTTCCGGCGACCGCATTTAACCCAG-----CTTGCT 423
QY 142 AsnProArgSerArgArgGlyIurYr---AsnGlnGlyLeuLeuAspAspGlnGluAlaThr 160
DB 424 TCCCGGCAAGTACAGCTGAGATTACAAAGGATTTACCGACATCGAGCTGACACG 483
QY 161 ValileThrAspVal----- 165
DB 484 CCGGAGCGTGTGGAATAACGCGCTCACCCCGAGCAAAATTGCGACTTGAAAGGA 543
QY 166 -----ProTrpAspIyValProGly-----Ala 173
DB 544 TTGATGGCGCAAAATCCGACAAATCCCTGCGCGCCCGGACATCGGGAACACACC 603
QY 174 LeuCyValleuGlnGlnGlyGlyGlnThrGlnileuValleuArgValGlyGluAlaLeu 193
DB 604 GTCAAGCTGTCTCAAGCAATTCGGGACGCGTGAAGAAAGTACTGCGATCGATGATGATC 663
QY 194 LeuIyGlnArgLeuProIySerPheIySerGln-----AspValleuValleuValMetAla 211
DB 664 AAAGGGGAGGAGCTGAAGAAATTTGCGCAATCCCGGATTTGGCCCTT---TTAAGC 720
QY 212 LeuAlaPheLeuAspValSerArgAspAla-----MetAlaLeuAspProProAsp 228
DB 721 AAACAGCTGGCCGCTATTGCGCGACGCCCGGTTGACCTGACCTGAT-----GAC 774
QY 229 PheileThrGlyIyrglnPheValGlnGlnAlaLeuIySleuLeuGlnGlnGlyAla 248
DB 775 ATTGTCTACAAAGAGAAAGACCGGGAAGAAAGTGTGCTTGTTCAGAGCTCGGATTC 834
QY 249 SerSerleuAlaProAspLeuArgAlaGlnileAspGlu----- 261
DB 835 CAGTGTCTTCGACAAAGATGCGCTCAACGAGTGAAGCGAAGCCGCTGCGCGG 894
QY 262 -----ThleuGlnGlnIleThrProArgTyrglnValleuGlnleuGlnleu 277
DB 895 ATGAGTTTTCGATCGCGACAGCGCTCACGAGCAAAATGCTCGCGCAAAAGCGGCCCTC 954
QY 278 -----ProleuGlyAspAspTyrglnAlaAlaIySleuAsnGlnleuSerGlyVala 294
DB 955 GTGCTGAGGTGTGGGAGCAACTATACATCCCGGATTTGCGGATGCGCT----- 1009
QY 294 IArgAsnIleleuTyrglnValGlyGlyAlaSer-AlaLeuValGlyIyLeuT 314
DB 1010 -----TGGCCAAAGAAAGCGCGGCTTTTCTGCGCCGAGACGCGGCTC 1056
QY 314 hrArgGlnIyPheMetAsnGlnAlaPhe----- 323
DB 1057 GCCGATCCGAATTTCTGCTTGGCTTGGCGATGACGAAAGAAACGATTTTGAT 1116
QY 324 -----LeuArgMetThrAlaAlaGlnGlnVal- 332

DB 1117 TCAAAGCGGCGCGCGCTGCGCTAAATGAGAAAGAAATGCAATGCGCGCGCTGCTTC 1176
QY 333 AspLeuPheValAlaThrProSerAsnIleProAlaGluSer----- 346
DB 1177 GATGTGCTGCTGCGCTTACTTGTGCTGATCCGCGGACGCGGCGGACGCTGCGCG 1236
QY 347 -----PheGlnValTyrglnValAlaLeuAlaLeuValAlaGlnAlaPheIleGlyIyS- 364
DB 1237 GTGGGAAATCATCATGACGAGCGCGCTGATGAGTGAAGCGGCTTATGAAAGGA 1296
QY 365 -----LysProHlSleuLeuGlnAspAlaAspIySleuGlnPheGln 377
DB 1297 GCGAAGCGGACGCTTCGATGACACGACGCTTCCGAGACATCTGCGCCG- 1347
QY 378 GlnleuGlnGlnAlaIyValMetAlaMetGlnIleProAlaMetLeuTyrglnThrArg 397
DB 1348 -----AAGCGCGCGCGCTTGGCGCTTGAAGCGCGTTCATGACGAACTGCGCGC 1401
QY 398 AsnAsnTPGlu---IleAspPheGlyleuGlnArgGlyLeuCyAlaLeuLeuIleGly 416
DB 1402 AACGAACAAAGTGGCTGCTGACCGAGCTCAACGCGCTGCGCATTTTGGCCAT 1461
QY 417 -----IyValAspGlnIyCySArgMet---TrpLeuGlyLeuAsp--- 428
DB 1462 ATGGAATTTACTGAGTGAAGTGAACAGAGCGGCTTGAACAGATGGGCGGAGCTC 1521
QY 429 SerGlnAspSerGlnTyrglnAsnProAlaIleValGlnPheValleuGlnAsnSerAsn 448
DB 1522 ACCGAGCAGCTGACG-----CGGTCGAGCGCGCGCATTTACGACTGCGCGG 1569
QY 449 ArgAspAspAsnAspAspLeuProGlyleuCySlySleuLeuGlnIyThrTrpLeuAlaGly 468
DB 1570 CAAAGTTCACATTAATCTGCGCG-----AAACGCTCGGAGCG----- 1608
QY 469 ValValPheProArgPheArgAspThrIySAspIySlyPheIySleuGlyAspTyrgln 488
DB 1609 GTTTATTTTGAACAGCTGACACTCCCGCTTGTGAAGAAAGCAAAACCGCGC---TATTCG 1665
QY 489 AspAspProMetValleuSerTyrgln---GlnArgValGlnValleuGlnIySerPro 507
DB 1666 ACTTCAGCGCGATGCTTGAAGACTTGCACCGCACCATCAATATCGTGAA-----CAT 1719
QY 508 LeuAlaAlaAlaAlaThrMetAlaArgIleGlyAlaGlnIySvalIySAlaSerAlaMet 527
DB 1720 ATTTGCAATTACCGCCCACTCGGACGTCGACGTCACAGTATATGAA---GGCTGCTG 1776
QY 528 GlnAlaLeuGlnIySValPheProSerArgTyrglnThrAspArgAsnSerAlaGluProIyS 547
DB 1777 AAAGTGTGACCGCGTGAACGCGGCAAGTGCACAGATTTCAATCAAGCGC----- 1827
QY 548 AspValGlnGlnIyThr-----ValPheSerValAspProValGlyAsnAsnValGlyArg 565
DB 1828 ---TTGACGCAAAAGCGCGCGCTCAGCTCGCTGCAACGCAATTTGCAAAATTCATTCGAT 1884
QY 566 AspGlyIyProGlyValPheIleAlaGlnAlaValArgProSerGlu----- 581
DB 1885 CCGCTTGAAGAAAGCGGAAATTCGCCAGCGCTTGTGCTGCGAGCGGACGCTGCTC 1944
QY 582 -----AsnPheGlnIyThrAsnAspTyrglnAlaIleArgAlaGlyValSerGluSer 597
DB 1945 ATCTTTCGCGCGCATTTTTCGCAAAATGAGCTGCGCGCTCTCGCCATATGCGGAA--- 2001
QY 598 SerValAspGlnIyThrIyValGlu----- 605
DB 2002 -----GATACCAATTTGATGAAGCTTCCGCGCGGCTTGAACATCATGCAAAACA 2055
QY 606 ---MetSerValAlaAspMetLeuIySglu-----AlaSerValIySleuAla 621
DB 2056 GCCATGCAATTTTTCATGTGACGCAAGAAAGACGTGACACGCAACATGCGCGCAAGCG 2115
QY 622 AlaGlyAlaAlaIleGlyleuIleSerleuPheSerGlnIyTyrglnPheIySleuSerSer 641

Db 2116 AAGCCGTCATTTTGGCATCGTACGGCATTAAGTAT--TACGGCTCGCGCAAAAC 2172
QY 642 SerSerheGlnArgIysAspMetValSerSerMetGluSerAspValAlaThrIleGly 661
Db 2173 TTGAACATTAAGCGCAAAAGCGCGCTGAATTTATGAGCATATTTTGCACGTTTCCA 2232
QY 662 SerValArgAlaAspAspSerGluAlaLeuProArgMetAspAlaArgThrAlaGluAsn 681
Db 2233 GGTCTAAG-----CAATATATGACAAAC 2256
QY 682 IleValSerIysTrpGlnIleIleYsSerIleuAlaPheGlyProAspHisArgIleGlu 701
Db 2257 ATTGTGCAGAA--GCGAAACAAAAGGATATGTGACGACGCTGCTGCATCGCGCGCC 2313
QY 702 MetLeuProGluValLeuAspGlyArgMet--LeuYsIleTrpThrAspArgAlaAla 720
Db 2314 TATTGCCCGATATTACAGCGCACTTCAAGTCCGACGCTCGCGAGCGGAGCGCG 2373
QY 721 ---GluThrAlaGlnLeuGlyLeuValTyrAspTyrThrLeuLeuIleYsLeuSerValAsp 739
Db 2374 ATGAACACACCGATCCAGGAGTGCCTGAT--ATTATTAAAAAGCATGATCGAT 2430
QY 740 ---SerValThrValSerAlaAspGlyThrArgAla----- 750
Db 2431 CTAAGCGTGAAGCTGCGCAAGAACGCGCTGCAGCGCGCTGTGCTGCAAGTCATGAC 2490
QY 751 -----LeuValGluAlaThrLeuGluGluSerAlaCysLeuSerAspLeuValHisPro 768
Db 2491 GAACCTCATTTTGAAGCGCGCGAAAGAGAAATCGAGCGGCTGTGCGCGCTCGTT---CCA 2547
QY 769 Glu 769
Db 2548 GAG 2550

Search completed: February 21, 2006, 13:54:46
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